



PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants : Jennifer L. Mitcham et al.
Application No. : 09/636,801
Filed : August 10, 2000
For : COMPOSITIONS AND METHODS FOR THERAPY AND
DIAGNOSIS OF OVARIAN CANCER

#13
Plunkett
1/5/0

Examiner : Mary K. Zeman
Art Unit : 1631
Docket No. : 210121.462C4
Date : December 17, 2001

Official Draftsperson
Commissioner for Patents
Washington, DC 20231

FILING FORMAL DRAWINGS

Commissioner for Patents:

Enclosed are 101 sheets of formal drawings, Figures 1A-25, for filing in the above-identified application.

Respectfully submitted,

Seed Intellectual Property Law Group PLLC

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Registration No. 42,676

Enclosures:

Formal Drawings (101 sheets, Figs. 1A-25)

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Fig. 1B

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11739-1&2

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11779.2.contig

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Fig. 1E

11781-76-87-37

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13697.1

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TAATGAGTGATATACATTACCTCTGTTCACTCACTATTGCCAGCACCAGTCACAAGGCCCCACCAAATACCAGAG
CCCAAGAAATGTAGTCCTGTTGATATGGTTTTGCTGTGTCCCAACCCAAATCTCATCTTGAATTGTAAGCTCCCAT
AATTCCTATGTGTTGTGGGAGGGACCTGGTG

Fig. 1H

13697.2

ATCATGAGGATGTTACCAAAGGGATGGTACTAAACCATTGTATTCTGCTGTTTTCACTGCTTTGAAGATACTA
CCTGAGACTGGGTAATTTATAAAACAAAAGAGATTTAATTGACTCACAGTTCTGCATGGCTGAAGAGGCCTCAGGAA
ACTTACAGTCATGGTGAAGGCAAAGGAGGAGCAAGGCATGTCTTACATGTCAGTAGGAGAGAGAGCGAGAGCAGG
AGAACCTGCCACTTATAAACCATTCAGATCTCATAACTCCCTATCATGAGAAAAACATGGAGGAAACCACTCAT
GATCCAATCACCTCCCGCCAGGTCCCTCCCTCGACACGTGGGGATTATAATTGAGGATTAGAGGGACACAGAGACA
AACCATATCATCATTCATGAGAAATCCACCTCATAGTCCAATCAGTCTCTACCAGGCCCCACCTCCAACACTGGG
GATTGCAATTCAACATGAGATTTGGATGGGGACACAGATTCAAACCATATCATAC

13699.1&2

CATGGCCTTTCTCCTTAGAGGCCAGAGGTGCTGCCCTGGCTGGGAGTGAAGCTCCAGGCACTACCAGCTTTCTGA
TTTTCCCGTTTGGTCCATGTGAAGAGCTACCACGAGCCCCAGCCTCACAGTGTCCACTCAAGGGCAGCTTGGTCTT
CTTGCTCTGCAGAGGCAGGCTGGTGTGACCTGGGAACCTGACCCGGAACAACAGGTGGCCCAGAGTGAGTGTGG
CCTGGCCCCCTCAACCTAGTGTCCGTCTCTCTCTCTGGAGCCAGTCTTGAGTTTAAAGGCATTAAGTGTTAGAT
ACAAGCTCCTTGTGGCTGGAAAAACACCCCTCTGCTGATAAAGCTCAGGGGGCACTGAGGAAGCAGAGGCCCCCTG
GGGGTGCCCTCCTGAAGAGAGCGTCAGGCCATCAGCTCTGTCCCTCTGGTCTCCACGTCTGTTCTCACCTCC
ATCTCTGGGAGCAGCTGCACCTGACTGGCCACGCGGGGCGAGTGGAGGCACAGGCTCAGGGTGGCCGGGCTACCTG
GCACCTATGGCTTACAAAGTAGAGTTGGCCAGTTTCTTCCACCTGAGGGGAGCACTCTGACTCCTAACAGTCT
TCCTTGCCCTGCCATCATCTGGGGTGGCTGGCTGTCAAGAAAGGCCGGGCATGCTTTCTAACACAGCCACAGGAG
GCTTGAGGGCATCTTCCAGGTGGGGAACAGTCTTAGATAAGTAAGGTGACTTGCCCTAAGGCCTCCAGCACCTT
TGATCTTGAGTCTCACAGCAGACTGCATGTSAACTGGAACCGAAAACATGCCTCAGTATAAAA

13703.3

CCAGAACCTCCTTCTCTTTGGAGAATGGGGAGGCCTCTTGAGACACAGAGGGTTTCACTTGGATGACCTCTAGA
GAAATTGCCAAGAAGCCACCTTCTGGTCCCAACCTGCAGACCCACAGCAGTCAGTTGGTCAGGCCCTGCTGTA
GAAGGTCACTTGGCTCCATTGCCTGCTTCCAACCAATGGGCAGGAGAGAAGGCCTTTATTTCTCGCCACCCATT
TCCTGTACCAGCACCTCCGTTTTAGTCAGYGTGTCCAGCAACGGTACCGTTTACACAGTCA

13705.1

TGCATGTAGTTTTATTTATGTGTTTTSGTCTGGAAAACCAAGTGTCCAGCAGCATGACTGAACATCACTCACTTC
CCCTACTTGATCTACAAGGCCAACGCCGAGAGCCCAGACCAGGATTCCAAACACACTGCACGAGAATATTGTGGAT
CCGCTGTCAGGTAAGTGTCCGTCACTGACCCARACGCTGTTACGTGGCACATGACTGTACAGTGCCACGTAAACAGC
ACTGTACTTTTCTCCCATGAACAGTTACCTGCCATGTATCTACATGATTGAGAACATTTTGAACAGTTAATTCTGA
CACTTGAATAATCCCATCAAAAACCGTAAAATCACTTTGATGTTTGTAAACGACAACATAGCATCACTTTACGACAG
AATCATCTGGAAAAACAGAACCAACGAATACATACATCTTAAAAATGCTGGGGTGGGCCAGGCACAGCTTCACGCC
TGTAATCCAGCACTTTGGGAGGCTTAAGCGGGTG

13705.2

TGGGGCGGAAAGAAGCCAAGGCCAAGGAGCTGGTGCGGCAGCTGCAGCTGGAGGCCGAGGAGCAGAGGAAGCAGAA
GAAGCGGCAGAGTGTGTGCGGCCCTGCACAGATACCTTCACTTGTCTGGATGGAAATGAAAATTACCCGTGTCTTGTG
GATGCAGACGGTGATGTGATTTCTTCCCAACATAACCAACAGTGAGAAGACAAAGGTTAAGAAAACGACTTCTG
ATTTGTTTTTTGGAAGTAACAAGTGCCACCAGTCTGCAGATTTGCAAGGATGTCATGGATGCCCTCATTCTGAAAAT
GGCAAGAAATGAAAAAGTACACTTTAGAAAATAAAGAGGAAGGATCACTCTCAGATACTGAAGCCGATGCAGTCTC
TGGACAACCTCCAGATCCCACAACGAATCCAGTGCTGGAAAGGACGGGGCCCTTCTTCTGGTGGTGGAACANGTC
CCGGTGGTGGATCTTGGAANGGAACCTGAANGTGGTGTACCCCGTCCAAGGCCGACCTTGCCAC

13707.4

TCCCGCGCTCGCAGGGCNCGTGCCACCTGCCYGTCCGCGCGCTCGCTCGCTCGCCCGCCGCGCCGCGCTGCCGACC
GYCAGCATGCTGCCGAGAGTGGGCTGCCCCGCGCTGCCGCTGCCGCGCCGCGCTGCTGCCGCTGCTGCCGCTGC
TGCTGCTGC

13708.1&2

GGCGGGTAGGCATGGAAGTGAAGAAGCAAGAAGCTTTCAGACTACGTGGGGAAGAATGAAAAACCAAATTAT
CGCCAAGATTCAGCAAAGGGGACAGGGAGCTCCAGCCGAGAGCCTATTATTAGCAGTGAGGAGCAGAAGCAGCTG
ATGCTGTACTATCACAGAAGACAAGAGGAGCTCAAGAGATTGGAAGAAAATGATGATGATGCCTATTTAACTCAC
CATGGGCGGATAACACTGCTTTGAAAAGACATTTTCATGGAGTGAAAGACATAAAGTGGAGACCAAGATGAAGTTC
ACCAGCTGATGACACTTCAAAGAGATTAGCTCACCT

13709.1

TCTGAAGGTAAATGTTTCATCTAAATAGGGATAATGRATAACACCTATAGCATAGAGTTGTTTGAGATTAAATGA
GATAATACATGTAAAATTATGTGCCTGGCATAACAGCAAGATTGTTGTTGTTGTTGATGATGATGATGATGATA
ATATTTTTCTATCCCAGTGCACAACCTGCTTGAACCTATTAGATAATCAATACATGTTTCTTGAAGTGAAGTCAAT
TTCCCATGTTGTCTGACTGATGAAGCCCTACATTTCTTCTAGAGGAGATGACATTTGAGCAAGATCTTAAAGAA
AATCAGATGCCTTCACCTGACCACTGCTTGGTGTATCCCATGGCACTTTGTACATCTCTCCATTAGCTCTCATCTCA
CCAGCCCATCATTATTGTATGTGCTGCCTTCTGAAGCTTGCAAGCTGGCTACCATCMGGTAGAATAAAAAATCATCCT
TTCATAAAATAGTGACCCTCCTTTTTTATTTGCATTTCCCAAAGCCAAGCACCGTGGGANGGTAG

13709.2

TATGAAGAAGGGAAAAGAAGATAATTTGTGAAAGAAATGGGTCCAGTTACTAGTCTTTGAAAAGGGTCAGTCTGTA
GCTCTTCTTAATGAGAATAGGCAGCTTTTCAGTTGCTCAGGGTCAGATTTCCCTAGTGGTGTATCTAATCACAGGAA
ACATCTGTGGTTCCTCCAGTCTCTTTCTGGGGGACTTGGGCCCATTCTCATTTTCAATTAATTAGAGGAAATAGA
ACTCAAAGTACAATTTACTGTTGTTTAAACAATGCCACAAAGACATGGTTGGGAGCTATTTCTTGATTTGTGTAAAA
TGCTGTTTTTGTGTGCTCATAATGGTTCCAAAAATTGGGTGCTGGCCAAAGAGAGATACTGTTACAGAAGCCAGCA
AGAAGACCTCTGTTCAATCACACCCCCGGGGATATCAGGAATTGACTCCAGTGTGTGCAAATCCAGTTTGGCCTAT
CTTCT

13712.1&2

TGAGGGACTGATTGGTTTGCTCTCTGCTATTCAATTCCTCAAGCCCACTTGTTCCCTGCAGCGTCCTCCTTCTCATT
CCCTTTAGTTGTACCCTCTCTTTTCATCTGAGACCTTTCCCTTCTTGATGTGCGCTTTTCTTCTTCTTGCTTTTTCTG
ATGTTCTGCTCAGCATGTTCTGGGTGCTTCTCATCTGCATCATTCCCTTCAGATGCTGTAGCTTCTTCCCTCCTCTT
TCTGCCTCCTTTTCTTTTTCTTTTTTTGGGGGGCTTGCTCTGACTGCAGTTGAGGGGGCCCCAGGGTCTGGCC
TTTGAGACGAGCCAGGAAGGCCTGCTCCTGGGCCTTAGGCGAGCAAGCTTGCCCTTCATTGTGATCCCAAGACGG
GCAGCCTTGTTGTGCTGTTGCGCCCTCACAGGCTTGAGCAGCATCTCATCAGTCAGAATCTTTGGGGACTTGACC
CCTGGTTGTCGTCATCACTGCAGCTCTCCAAGTCTTTGTTTGGCTTCTCTCCACCTGAAGTCAATGTAGCCATCTT
CACAACTTCTGATACAGCAAGTTGGGCTTGGGATGATTATAACGGGTGGTCTCCTTAGAAAGGCTCCTTATCTGT
ACTCCATCCTGCCAGTTTCCACTACCAAGTTGGCCGAGTCTTGTTGAAGAGCTCATTCCACCAGTGGTTTGTGA
ACTCCTTGGCAGGGTCATGTCCTACCCCATGAGTGTCTTGCTTCAGYGTACCCTGAGAGCCTGAGTGATACCATT
CTCCTTCCG

13714.1&2

GACAACATGAAATAAATCCTAGAGGACAAAATTAACCTCAATAGAGTGTAGTCTAGTTAAAACTCGAAAAATGAG
CAAGTCTGGTGGGAGTGGAGGAAGGGCTATACTATAAATCCAAGTGGGCCTCCTGATCTTAACAAGCCATGCTCAT
TATACACATCTCTGAAGTGGACATACCACCTTTACGCAGGAAACAGGGCTTGGAAGTCTAAGGGAAATTAACATG
CACCACCCACATCTAACCTACCTGCCGGGTAGGTACCATCCCTGCTTCGCTGAAATCAGTGCTC

13716.1&2

TTGGAATTAAATAAACCTGGAACAGGGAAGGTGAAAGTTGGAGTGAGATGTCTTCATATCTATACCTTTGTGCAC
AGTTGAATGGGAAGTGTGTTGGGTTAGGGCATCTTAGAGTTGATTGATGGAAAAAGCAGACAGGAAGTGGTGGGAG
GTCAAGTGGGGAAGTTGGTGAATGTGGAATAACTTACCTTTGTGCTCCACTTAAACCAGATGTGTTGCAGCTTTCC
TGACATGCAAGGATCTACTTTAATTCCACACTCTCATTAAATAAATTGAATAAAAGGGAATGTTTTGGCACCTGATA
TAATCTGCCAGGCTATGTGACAGTAGGAAGGAATGGTTTCCCCTAACAAAGCCCAATGCACTGGTCTGACTTTATAA
ATTATTTAATAAAATGAAGTATTATC

13718.2

AAACTGGACCTGCAACAGGGACATGAATTTACTGCARGGTCTGAGCAAGCTCAGCCCCCTACCTCAGGGCCCCAC
AGCCATGACTACCTCCCCAGGAGCGGGAGGGTGAAGGGGGCCTGTCTCTGCAAGTGGAGCCAGAGTGGAGGAATG
AGCTCTGAAGACACAGCACCCAGCCTTCTCGCACCAGCCAAGCCTTAACCTGCCTGACCCTGAACCAGAACCC
AGCTGAACTGCCCCCTCAAGGGACAGGAAGGCTGGGGGAGGGAGTTTACAACCAAGCCATTCCACCCCCTCCCCT
GCTGGGGAGAATGACACATCAAGCTGCTAACAATTGGGGGAAGGGGAAGGAAGAAAACCTCTGAAAACAAAATCTTG
T

13722.3

CATGCGTTTTACCACTGTTGGCCAGGCTGGTCTCGAACTCCTGGCCTCAAGCAATCCACCCGCCTCAGCCTCCAAA
AGTGCTGGGATTACAGATGTGAGCCATGGCACCATGCCAAAAGGCTATATTCTGGCTCTGTGTTTCCGAGACTGC
TTTTAATCCCAACTTCTCTACATTTAGATTAATAAATATTTTATTCATGGTCAATCTGGAACATAATTACTGCATC
TTAAGTTTCCACTGATGTATATAGAAGGCTAAAGGCACAATTTTTATCAAATCTAGTAGAGTAACCAAACATAAAA
TCATTAATTACTTTCACTTAATACTAATTGACATTCTCAAAGAGCTGTTTTCAATCCTGATAGGTTCTTTAT
TTTTTCAAATATATTTGCCATGGGATGCTAATTTGCAATAAGGCGCATAATGAGAATACCCCAAACCTGGA

13722.4

GTTGGACCCCCAGGGACTGGAAAGACACTTCTTGCCCCGAGCTGTGGCGGGAGAAGCTGATGTTCTTTTTATTATG
CTTCTGGATCCGAATTTGATGAGATGTTTGTGGGTGTGGGAGCCAGCCGTATCAGAAATCTTTTTAGGGAAGCAAA
GGCGAATGCTCCTTGTGTTATATTTATTGATGAATTAGATTCTGTTGGTGGGAAGAGAATTGAATCTCCAATGCAT
CCATATTCAAGGCAGACCATAAATCAACTTCTTGCTGAAATGGATGGTTTTAAACCCAATGAAGGAGTTATCATAA
TAGGAGCCACAACTTCCCAGAGGCATTAGATAATGCCTTAATACCGTCCTGGTCGTTTTGACATGCAAGTTACAG
TTCCAAGGCCAGATGTAAAAGGTGCAACAGAAATTTTGAAATGGTATCTCAATAAAATAAAGTTTGATCAATCCCG
TTGATCCAGAAATTATAGCCTCGAGGTACTGGTGGCTTTTCCGGAAGCAGAGTTGGGAGAATCTT

13724-13698-13748

GCCTACAACATCCAGAAAGAGTCTACCCTGCACCTGGTGCTSCGTCTCAGAGGTGGGATGCAGATCTTCGTGAAGA
CCCTGACTGGTAAGACCATCACTCTCGAAGTGGAGCCGAGTGACACCATYGAGAACGTCAAAGCAAAGATCCARGA
CAAGGAAGGCRTYCCTCCTGACCAGCAGAGGTTGATCTTTGCCGAAAGCAGCTGGAAGATGGDCGCACCCTGTCT
GACTACAACATCCAGAAAGAGTCYACCCTGCACCTGGTGCTCCGTCTCAGAGGTGGGATGCARATCTTCGTGAAGA
CCCTGACTGGTAAGACCATCACCTCGAGGTGGAGCCAGTGACACCATCGAGAATGTCAAGGCAAAGATCCAAGA
TAAGGAAGGCATCCCTCCTGATCAGCAGAGGTTGATCTTTGCTGGGAAACAGCTGGAAGATGGACGCACCCTGTCT
GACTACAACATCCAGAAAGAGTCCACTCTGCACTTGGTCTGCGCTTGAGGGGGGGTGTCTAAGTTTCCCCTTTTA
AGGTTTCAACAAATTTTATTGCACTTTCTTTCAATAAAGTTGTTGCATTCCC

13730.1

GAAGTGGGCCCCTGAGCCCAAGTCATGCCTTGTGTCCGCATCTGCCGTGTCACCTCTGTCCTGCCCTCACCCCTC
CCTCCTGGTCTTCTGAGCCAGCACCATCTCCAAATAGCCTATTCTTCTGCAAATCACACACACATGCGGGCCAC
ACATACCTGCTGCCCTGGAGATGGGGAAGTAGGAGAGATGAATAGAGGCCCATACATTGTACAGAAGGAGGGGCAG
GTGCAGATAAAAGCAGCAGACCCAGCGGCAGCTGAGGTGCATGGAGCACGGTTGGGGCCGGCATTGGGCTGAGCAC
CTGATGGGCCCTCATCTCGTGAATCCTCGAGGCAGCGCCACAGCAGAGGAGTTAAGTGGCACCTGGGCGGAGCAGAG
CAGGAGACTGAGGGTCAGAGTGGAGGCTAAGCTGCCCTGGAACCTCAATCTTGCCTGCCCCCTAGTATGAAGCC
CCCTTCTGCCCTACAATTCCTGA

13732.1

ATGGATCTTACTTTGCCACCCAGGTTGGAGTGCAGTGCCTGCAATCTTGGCTCACTGCAGCCTTAACCTCCCAGGCT
CAAGCTATCCTCCTGCCAAAGCCTTCCACATAGCTGGGACTACAGGTACACNGCCACCACACCCAGCTAAAATTTT
TGTATTTTTTTGTAGAGACGGGATCTCGCCACGTTGCCAGGCTGGTCCCATCCTGACCTCAAGCAGATCTGCCAC
CTCAGCCCCCAACGTGCTAGGATTACAGGCGTGAGCCACCGCACCCAGCCTTTGTTTTGCTTTTAATGGAATCAC
CAGTTCCTCCTCGTGTCTCAGCAGCAGCTGTGAGAAATGCTTTGCATCTGTGACCTTTATGAAGGGGAACCTCCAT
GCTGAATGAGGGTAGGATTACATGCTCCTGTTTCCCGGGGTCAAGAAAGCCTCAGACTCCAGCATGATAAGCAGG
GTGAG

13732.2

ATAGGGGCTTTAAGGAGGGAATTCAGGTTCAATGAGGTCGTAAGGCCAGGGCTCTTATCCAGTAAGACTGGGGTCC
TTAGATGAGAAAGAGACACCCGAGGTCCTTCTCTCTGCCGTGTGAGGATGCATCAAGAAGGCGGCCGTCTGCAAGC
GAAGGAGAGGCCGCACCAGAAACCGACACCTTCATCTTGGACTTGACGCTCTAGAACTGAGAAAATAACTGTCTG
TTGGTTAAGCCACCCAGTTTGTAGTATTCTCTTATGGCTTCCTAAGCAGACTAACAAACAAACACCCAAAATTAAC
TGATGGCTTCGCTGTCTTCTGTAAAAATTGCTATGAGAGAACTTTTCACTCACTGTTTTGCAGTTTCTCCCTCAGT
CCCTGGTTCTTTCTTCTCACATAATCCCAATTTCAATTTATAGTTTCATGGCCAGGCAGAGTCATTTCATCACGGCA
TCTCCTGAGCTAAACCAGCACCTGCTCTGCTCACTTCTTGACTGGCTGCTCATCATCAGCCCTCTTGAGAGATTT
CATTTCTCCCGTGCCAGGTAATTCACGCACCAAGCTCA

13735.1

GGATAATGAAGTTGTTTTATTTAGCTTGGACAAAAAGGCATATTCCTCTATTTTCTTATACAACAAATATCCCCAA
AATAAGCAAGCATATATATCTTGAATGTGTAATAATCCAGTGATAAAACAAGAGCAGTACTTTAAAAGAAAAAAA
ATATGTATTTCTGTCAAGTTAAAATGAGAATCAAAACCATTTACTCTGCTAACTCATTATTTTTGCTTTCTTTTT
GGTTAAGAGAGGCAATGCAATACACTGAAAAAGTTTTATCTTATCTGGCATTGGAATTAGACATATTCAAACCC
CAGCCCCCATTTCCAAACTTTAAGACCACAAACAAGTAATTTACTTTTTCTGAACATTGGTTTTTTCTGGAAAATGG
GAATTATAAAATAGACTTTGCAGACTCTTATGAGATTAAATAAGATAATGTATGAAATTCCTTCTTTTTTACT
TCTTTTCTTTTTGAGATGGAGTCTCACCCCGTCACCCAGGCTGGAGTACAGTG

13735.2

CCACTGCACTCCAGCCTGGGTGACGGAGTGAGACTCTGTCTCAAAAAACAAACAAACAAACAAACAAAACTGA
AAAGGAAATAGAGTTCCTCTTTCCTCATATATGAATATATTATTTCAACAGATTGTTGATCACCTACCATATGCTT
GGTATTGTTCTAATTGCTGGGGATACAGCAAGAGGTTCTGCAGAACTTCATGGAGCATGAAAGTAAATAAACAAAG
TTAATTTCAAGGCCAGGCATGGTTGCTCACACCTTTAGTCCCAGCACTTTGGGAGGCTGAGGCAGGTGGATCACTT
GGGCCCAGGAGTTCAAGGCTGCAGTGAGCCAAGATTGTGCCACTACTCTCCAGGCTGGGCAACAGAGCAAGACCTT
GTCTCAGGGGGAACAAAAAGTTAATTTAGATTGTTAAGTGCTGTAAAGGAAGTAAATAGGTTGATATTCAAGA
GAGCACCTGAAGGCCAGGCGTGGTGGCTCACGCCTGTGGTCTAACGCTTTGGGAAGCCCGAGCGGGCGGATCACAA
GGTCAGGAGAATTTTGGCCAGGCATGGTG

13736.1

AGAATCCATTTATTGGGTTTTAACTAGTTACACAACCTGAAATCAGTTTGGCACTACTTTATACAGGGATTACGCC
TGTGTATGCCGACACTTAAATACTGTACCAGGACCACTGCTGTGCTTAGGTCTGTATTCAGTCATTCAGCATGTAG
ATACTAAAAATATACTGTAGTGTTCTTTAAGGAAGACTGTACAGGGTGTGTTGCAAGATGACATTCACCAATTTG
TGAATTATTTCAACCCAGAAGATACCTTTCACTCTATAAACTTGTCTATAGGCAAACATGTGGTGTTAGCATTGAGA
GATGCACACAAAAATGTTACATAAAAGTTTACAGACATTCTAATGATAAGTGAACCTGAAAAAAAAAAAAACCCACAT
CTCAATTTTTGTAACAAGATAAAGAAAATAATTTAAAAACACAAAAAATGGCATTCACTGGGTACAAAGCC

13737.1&2

CAAATATTTAATATAAATCTTTGAAACAAGTTCAGAKGAAATAAAAAATCAAAGTTTGCAAAAACGTGAAGATTAAC
TTAATTGTCAAATATTCCTCATTGCCCCAAATCAGTATTTTTTTTATTTCTATGCAAAAGTATGCCTTCAAACCTGC
TTAAATGATATATGATATGATACACAAACCAGTTTTCAAATAGTAAAGCCAGTCATCTTGCAATTGTAAGAAATAG
GTAAAAGATTATAAGACACCTTACACACACACACACACACACACACACAGTGTGCACCGCCAATGACAAAAAACA
ATTTGGCCTCTCTAAAATAAGAACATGAAGACCCTTAATTGCTGCCAGGAGGGAACACTGTGTCACCCCTCCCTA
CAATCCAGGTAGTTTTCTTTAATCCAATAGCAAATCTGGGCATATTTGAGAGGAGTGATTCTGACAGCCACSGTTG
AAATCCTGTGGGGAACCATTCATGTCCACCCACTGGTGCCCTGAAAAAATGCCAATAATTTTTGCTCCCACTTCT
GCTGCTGTCTCTTCCACATCTCACATAGACCCCGAGCCCGCTGGCCCTGGCTGGGCATCGCATTGCTGGTAGAG
CAAGTCATAGGTCTCGTCTTTGACGTCACAGAAGCGATACACCAAATTGCCTGGTGGTCATTGTCATAACCAG

Fig. 1N

13738.1

TTTGACTTTAGTAGGGGTCTGAACTATTTATTTTACTTTGCCMGTAAATTTARACCYTATATATCTTTCATTATG
CCATCTTATCTTCTAATGBCAAGGGAACAGWTGCTAAMCTGGCTTCTGCATTWATCACATTA AAAATGGCTTTCTT
GGAAAATCTTCTTGATATGAATAAAGGATCTTTTAVAGCCATCATTTAAAGCMGNTTCTCTCCAACACGAGTCTG
CTSASGGGGGGKGAGCTGTGAACTCTGGCTGAAGGCTTTCCCATACACACTGCAATGACMTGGTTTCTGACCAGBG
TGAGTTA

13738.2

AGAGAAGCCCCATAAATGCAATCAGTGTGGGAAGGCCTTCAGTCAGAGCTCAAGCCTTTTCTCCATCATCGGGTT
CATACTGGAGAGAAACCCTATGTATGTAATGAATGCGGCAGAGCCTTTGGTTTTAACTCTCATCTTACTGAACACG
TAAGGATTCACACAGGAGAAAAACCCTATGTTTGTAATGAGTGCAGCAAGCCTTTTCGTCGGAGTTCCACTCTTGT
TCAGCATCGAAGAGTTCACACTGGGGAGAAGCCCTACCACTGCGTTGAATGTGGGAAAGCTTTTCAGCCAGAGCTCC
CAGCTCACCTACATCAGCCGAGTTCACACTGGAGAGAAGCCCTATGACTGTGGTGACTGTGGGAAGGCCTTCAGC
CGGAGGTCAACCCTCATTACAGCATCAGAAAGTTCACAGCGGAGAGACTCGTAAGTGCAGAAAAACATGGTCCAGCCT
TTGTTTCATGGCTCCAGCCTCACAGCAGATGGACAGATTCCCACTGGAGAGAAGCACGGCAGAACCTTTAACCATGG
TGCAATCTCATTCTGCGCTGGACAGTTC

13739.1&2

GAGACAGGGTCTCACTTTGTCACCCAGGCTGGAATGCAGTGGTGCGATCTTACGTAGCTCACTGCAGCCCTGACCT
CCTGGACTCAAACAATTCTCCTGCCTCAGCCCTGCAAGTAGCTGGGACTGTGGGTGCATGCCACCATGCCTGGCTA
ACTTTTGTAGTTTTTGTAAAGATGGGGTTTTGCCATGTTGCACATGCTGGTCTTGAACCTCTGAGCTCAAACGATC
TGCCACCTCGGCCTCCAGAAATGTTGGGATTACAGGGGTAAACCACCACGCCTGGCCCCATTAGGGTATTCTTAG
CATCCACTTGCTCACTGAGATTAATCATAAGAGATGATAAGCACTGGAAGAAAAAAATTTTACTAGGCTTTGGAT
ATTTTTTCTTTTTTCAGCTTTATACAGAGGATTGGATCTTTAGTTTTCTTTAACTGATAATAAACATTGAAAG
GAAATAAGTTTACCTGAGATTCACAGAGATAACCGGCATCACTCCCTTGCTCAATTCCAGTCTTTACCACATCAAT
TATTTTCAGAGGTGCAGGATAAAGGCCTTTAGTCTGCTTTGCACTTTTTCTTCCACTTTTTTGTAAACCTGTTGC
CTGACAAATGGAATTGACAGCGTATGCCATGACTATTCCATTTGTGAGGCATACGCTGTCAATTTTTCCACCAATC
CCTTGTCTCTCTTTGGAGAGATCTTCTTATCAGCTAGTCCTTTGGCAAAAGTAATTGCAACTTCTTCTAGGTATTC
TATTGTCCGTTCCACTGGTGGAAACCCTGGGACCAGGACTAAAACCTCCAG

13741.1

ATCTCATATATATATTTCTTCCTGACTTTATTTGCTTGCTTCTGNACGCATTTAAAATATCACAGAGACCAAAAT
AGAGCGGCTTTCTGGTGGAACGCATGGCAGTCACAGGACAAAATACAAAACCTAGGGGGCTCTGTCTTCTCATACAT
CATACAATTTTCAAGTATTTTTTTATGTACAAAGAGCTACTCTATCTGAAAAAAATTA AAAAATAAATGAGACA
AGATAGTTTATGCATCCTAGGAAGAAAGAATGGGAAGAAAGAACGGGGCAGTTGGGTACAGATTCTGTCCCCTGT
TCCCAGGGACCACTACCTTCCTGCCACTGAGTTCCCCACAGCCTCACCCATCATGTACAGGGCAAGTGCCAGGG
TAGGTGGGGACCACTGGAGACAGGAACCAGCAACATACTTTGGCCTGGAAGATAAGGAGAAAGTCTCAGAAACACA
CTGGTGGGAAGCAATCCACNGGCCGTGCCCCANGAGCTTCCACCTGCTGCTGGCTCCCTGGGTGGCTTTGGGAA
CAGCTTGGGCAGGCCCTTTTGGGTGGGNCCAACCTGGGCCTTTGGGCCGTGTGGAAAG

Fig. 10

13742.1

AAACATTGAGATGGAATGATAGGGTTTCCCAGAATCAGGTCCATATTTTAACTAAATGAAAATTATGATTTATAGC
CTTCTCAAATACCTGCCATACTTGATATCTCAACCAGAGCTAATTTTACCTCTTTACAAATTAAATAAGCAAGTAA
CTGGATCCACAATTTATAATACCTGTCAATTTTTCTGTATTAAACCTCTATCATAGTTTAAAGCCTATTAGGGTAC
TTAATCCTTACAAATAAACAGGTTTAAATCACCTCAATAGGCAACTGCCCTTCTGGTTTTCTTCTTTGACTAAAC
AATCTGAATGCTTAAGATTTTCCACTTTGGGTGCTAGCAGTACACAGTGTTACACTCTGTATTCCAGACTTCTTAA
ATTATAGAAAAAGGAATGTACACTTTTTGTATTCTTCTGAGCAGGGCCGGGAGGCAACATCATCTACCATGGTAG
GGACTTGTATGCATGGACTACTTTA

14351.1

ACTCTGTCGCCCAGGCTGGAGCCCBATGGMCGCATCTCGACTCCCTGCAAGCTMCGCCTCACAGGWTGATGCCATT
CTCCTGCCTCAGCATCTGGAGTAGCTGGGACTACAGGCGCCAGCCACCATGCCAGCTAATTTTT

14351.2

ACCTTAAAGACATAGGAGAATTTATACTGGGAGAGAAAGCTTACAAATGTAAGGTTTCTGACAAGACTTGGGAGTG
ATTCACACCTGGAACAACATACTGGACTTCACACTGGABAGAAACCTTACAAGTGTAAATGAGTGTGGCAAAGCCTT
TGGCAAGCAGTCAACACTTATTCACCATCAGGCAATTCA

14354.2

AGTCAGGATCATGATGGCTCAGTTTCCCACAGCGATGAATGGAGGGCCAAATATGTGGGCTATTACATCTGAAGAA
CGTACTAAGCATGATAAACAGTTTGATAACCTCAAACCTTCAGGAGGTACATAACAGGTGATCAAGCCCGTACTT
TTTTCTACAGTCAGGTCTGCCGGCCCCGGTTTTAGCTGAAATATGGGCCTTATCAGATCTGAACAAGGATGGGAA
GATGGACCAGCAAGAGTTCTCTATAGCTATGAACTCATCAAGTTAAAGTTGCAGGGCCAACAGCTGCCTGTAGTC
CTCCCTCCTATCATGAAACAACCCCTATGTTCTCTCCACTAATCTCTGCTCGTTTTGGGATGGGAAGCATGCCCCA
ATCTGTCCATTCATCAGCCATTGCCTCCAGTTGCACCTATAGCAACACCCTTGTCTTCTGCTACTTCAGGGACCAG
TATTCCTCCCTAATGATGCCTGCT

14354.1

CTTTGATTTTCTTCAATTTGTACGTTTGATTTTATGAAGTTGTTCAAGGGCTAACTGCTGTGTATTATAGCTTT
CTCTGAGTTCCTTCAGCTGATTGTTAAATGAATCCATTTCTGAGAGCTTAGATGCAGTTTCTTTTTCAAGAGCATC
TAATTGTTCTTTAAGTCTTTGGCATAATTCTTCTTTCTGATGACTTTCTATGAAGTAACTGATCCCTGAATCA
GGTGTGTTACTGAGCTGCATGTTTTAATTCTTTCGTTTAAATAGCTGCTTCTCAGGGACCAGATAGATAAGCTTAT
TTTGATATTCCTTAAGCTCTTGGTGAAGTTGTTGATTTCCATAATTTCCAGGTCACACTGGTTATCCCAAACCTC
T

16431.1.2

TGGAGGTGAAACGGAGGCAAGAAAGGGGGCTACCTCAGGAGCGAGGGACAAAGGGGGCGTGAGGCACCTAGGCCGC
GGCACCCCGGCGACAGGAAGCCGTCCTGAACCGGGCTACCGGTAGGGGAAGGGCCCGCTAGTCCTCGCAGGGCC
CCAGAGCTGGAGTCGGCTCCACAGCCCCGGGCGCTCGGCTTCTCACTTCTTGACCTCCCCGGCGCCCGGGCCTGA
GGACTGGCTCGGCGGAGGGAGAAGAGGAAACAGACTTGAGCAGCTCCCCGTTGTCTCGCAACTCCACTGCCGAGGA
ACTCTCATTTCTTCCCTCGCTCCTTACCCCCACCTCATGTAGAAAGGTGCTGAAGCGTCCGGAGGGAAGAAGAA
CCTGGGCTACCGTCCTGGCCTTCCMCCCCCTTCCCGGGCGCTTTGGTGGGCGTGAGATTGGGGTTGGGGGGGTG
GGTGGGGGTTCTTTTTTGGAGTGCTGGGGAACTTTTTCCCTTCTTCAGGTCAGGGGAAAGGGAATGCCAATTCA
GAGAGACATGGGGGCAAGAAGGACGGGAGTGGAGGAGCTTCTGGAACTTTGACCGCTCATCGGGAGGCGGCAGCT
CTAACAGCAGAGAGCGTCACCGCTTGGTATCGAAGCACAAGCGGCATAAGTCCAAACACTCCAAAGACATGGGGTT
GGTGACCCCGAAGCAGCATCCCTGGGCACAGTTATCAAACCTTTGGTGGAGTATGATGATATCAGCTCTGATTCC
GACACCTTCTCCGATGACATGGCCTTCAAACCTAGACCGAAGGGAGAACGACGAACGTCTGGATCAGATCGGAGCG
ACCGCCTGCACAAACATCGTCACCACCAGCACAGGCGTTCCCGGACTTACTAAAAGCTAAACAGACCG

16432-1

GACATGTTTGCCTGCAGGGGACCAGAGACAATGGGATTAGCCAGTGCTCACTGTTCTTTATGCTTCCAGAGAGGAT
GGGGACAGCTCTCAGGTGAGAATCCAGGCTGAGAAGGCCATGCTGGTTGGGGGCCCCCGGAAGCACGGTCCGGATC
CTCCCTGGCATCAGCGTAGACCCGCTGCTCAGGCTTGGGGTACCAAACTCATGCTCTGTACTGTTTTGGCCCCATG
CGGTGAGAGGAAAACCTAGAAAAAGATTGGTCTGTCTAAGGAATCAGCTGCCCCCTCATCCTCCGCATCCAATGCT
GGTGACAACATATTCCCTCTCCAGGACACAGACTCGGTGACTCCACACTGGGCTGAGTGGCCTCTGGAGGCTCGT
GGCCTAAGGCAGGGCTCCGTAAGGCTGATCGGCTGAACTGGGTGGGGTGAGGGTTTCTGACCCTTCGCTTCCCATC
CCATAACCGCTGTCAATGAGCTCACACTGTGGTCA

16432-2

GATGGCATGGTCGTTGCTAATGTGCCTGCTGGGATGGAGCACTTCTCCTGTGAGCCCAGGGGACCCGCCTGTCCC
TGGAGCTTGGGGCAAGGAGGGAAGAGTGATACCAGGAAGGTGGGGCTGCAGCCAGGGGCCAGAGTCAGTTCAGGGA
GTGGTCCTCGGCCCTCAAAGCTCCTCCGGGGACTGCTCAGGAGTGATGGTGCCCTGGAGTTTGGCCCAACTTCCCT
GGCCACCCTGGAAGGTGCCTGGCTGCTCCAGGCCCTTAGGCTGGGCTGATGGGTTTCTCCAGGACACAAGTATCAT
TAAAGCCACCCTCTCCTCAGCTTGTGAGGCCGCACATGTGGGACAGGCTGTGCTCACAACCCCTCGCCTGCCCTG
CCCTCCATCAGGAGGAGCCAGTGGAACCTTCGAAAAGCTCCAGCATCTCAGCAGCCCTCAAAAGTCGTCTGGGG
CAAGCTCTGGTTCTCCTGACTGGAGGTCATCTGGGCTTGGCCTGCTCTCTCTCG

17184.3

TAAAAAAGTGTAACAAAGGTTTATTTAGACTTTCTTCATGCCCCAGATCCAGGATGTCTATGTAAACCGTTATCT
TACAAAGAAAGCACAATATTTGGTATAAACTAAGTCAGTGACTTGCTTAAGTGAATAGCGTCCATCCAAAAGTGG
GTTTAAGGTAAAACTACCTGACGATATTGGCGGGGATCCTGCAGTTTGGACTGCTTGCCGGGTTTGTCCAGGGTTC
CGGGTCTGTTCTTGGCACTCATGGGGACAGGCATCCTGCTCGTCTGTGGGGCCCCGCTGGAGCCCTTACGTGAAGC
TGAAGGTATCGACCSTAGGGGGCTCTAGGGCAGTGGGACCTTCATCCGGAACATAACAAGGGTCGGGGAGAGGCCTC
TTGGGCTATGTGGG

Fig. 1Q

17184.4

CAAGCGTTCCTTTATGGATGTAAATTCAAACAGTCATGCTGAGCCATCCCGGGCTGACAGTCACGTTWAAGACACT
AGGTCGGGCGCCACAGTGCCACCCAAGGAGAAGAAGAATTTGGAATTTTCCATGAAGATGTACGGAAATCTGATG
TTGAATATGAAAATGGCCCCCAAATGGAATTCAAAAGGTTACCACAGGGGCTGTAAGACCTAGTGACCTCCTAA
GTGGGAAAGAGGAATGGAGAATAGTATTTCTGATGCATCAAGAACATCAGAATATAAACTGAGATCATAATGAAG
GAAAATTCATATCCAATATGAGTTTACTCAGAGACAGTAGAACTATTCCCAGG

17185.1

TAGGAATAACAAATGTTTATTCAGAAATGGATAAGTAATACATAATCACCTTCATCTCTTAATGCCCCTTCCTCT
CCTTCTGCACAGGAGACACAGATGGGTAAACATAGAGGCATGGGAAGTGGAGGAGGACACAGGACTAGCCACCACC
TTCTCTTCCCGGTCTCCAAGATGACTGCTTATAGAGTGGAGGAGGCAAACAGGTCCCCTCAATGTACCAGATGGT
CACCTATAGCACAGCTCCAGATGGCCACGTGGTTGCAGCTGGACTCAATGAACTCTGTGACAACCAGAAGATAAC
CTGCTTTGGGATGAGAGGGAGGATAAAGCCATGCAGGGAGGATATTTACCATCCCTACCCTAAGCACAGTGCAAGC
AGTGAGCCCCCGGCTCCAGTACCTGAAAAACCAAGGCCTACTGNCTTTTGGATGCTCTCTTGGGCCACG

17188.2

AAGCCTCCTGCCCTGGAAATCTGGAGCCCCCTTGGAGCTGAGCTGGACGGGGCAGGGAGGGGCTGAGAGGCAAGACC
GTCTCCCTCCTGCTGCAGCTGCTTCCCCAGCAGCCACTGCTGGGCACAGCAGAAACGCCAGCAGAGAAAATGGGAG
CCGAGAGTCTTAGCCCTGGAGCTGAGGCTGCCTCTGGGCTGACCCGCTGGCTGTACGTGGCCAGAACTGGGGTTG
GCATCTGGCATCCATTTGAGGCCAGGGTGGAGGAAAGGGAGGCCAACAGAGGAAAACCTATTCCTGCTGTGACAAC
ACAGCCCTTGTCACGCAGCCTAAGTGCAGGGAGCGTGATGAAGTCAGGCAGCCAGTCGGGGAGGACGAGGTAAC
TCAGCAGCAATGTCACCTTGAGCCTATGCGCTCAATGGCCCGGAGGGGCAGCAACCCCCCGCACACGTGAGCCAA
CAGCAGTGCTCTGCAGGCACCAAGAGAGCGATGATGGACTTGAGCGCCGTGTTT

17190.1

GTTTGGCAGAAGACATGTTTAATAACAFTTTTCATATTTAAAAAATACAGCAACAATTCTCTATCTGTCCACCATCT
TGCCTTGCCCTTCTGGGGCTGAGGCAGACAAAGGAAAGGTAATGAGGTTAGGGCCCCCAGGCGGGCTAAGTGCTA
TTGGCCTGCTCCTGCTCAAAGAGAGCCATAGCCAGCTGGGCACGGCCCCCTAGCCCCCTCAGGTTGCTGAGGCGGC
AGCGGTGGTAGAGTTCTTCACTGAGCCGTGGGCTGCAGTCTCGCAGGGAGAACTTCTGCACCAGCCCTGGCTCTAC
GGCCCGAAAGAGGTGGAGCCCTGAGAACCGGAGGAAAACATCCATCACCTCCAGCCCCCTCAGGGCTTCTCCTCT
TCCTGGCCTGCCAGTTCACCTGCCAGCCGGGCTCGGGCCGCCAGGTAGTCAGCGTTGTAGAAGCAGCCCTCCGAG
AAGCCTGCCGGTCAAATCTCCCCGCTATAGGAGCCCCCGGGAGGGGTGAGCACC

Fig. 1R

17190.2

CAAGTTGAACGTCAGGCTTGGCAGAGGTGGAGTGTAGATGAAAACAAAGGTGTGATTATGAAGAGGATGTGAGTCC
TTTGGGTGTAGGAGAGAAAGGCTGTTGAGCTTCTATTTCAAGATACTTTTACCTGTGCAAAAAGCACATTTTCCAC
CTCCTTCTCATGGCATTGTGTAAAGGTGAGTATGATTCCATTCCATCTGCATTTTAGAGGTGAAGAATAACGTAC
AAGGGATTCAGTGATTAGCAAGGGACCCCTCACTAAGTGTGATGGAGTTAGGACAGAGCTCAGCTGTTTGAATCT
CAGAGCCCAGGCAGCTGGAGCTGGGTAGGATCCTGGAGCTGGCACTAATGTGAGGTGCATTCCCTCCAACCCAGGC
TCAGATCCGGAACCTGACCGTGCTGACCCCCGAAGGGGAGGCAGGGCTGAGCTGGCCCGTTGGGCTCCCTGCTCCT
TTCACACCACACTCTCGCTTTGAGGTGCTGGGCTGGGACTACTTCACAGAGCAGC

17191.2&89.2

TGGCCTGGGCAGGATTGGGAGAGAGGTAGCTACCCGGATGCAGTCCTTTGGGATGAAGACTATAGGGTATGACCCC
ATCATTTCCCCAGAGGTCTCGGCCTCCTTTGGTGTTGAGCAGCTGCCCTGGAGGAGATCTGGCCTCTCTGTGATT
TCATCACTGTGCACACTCCTCTCCTGCCCTCCACGACAGGCTTGCTGAATGACAACACCTTTGCCAGTGCAAGAA
GGGGGTGCGTGTGGTGAAGTGTGCCCGTGGAGGGATCGTGGACGAAGGCGCCCTGCTCCGGGGCCCTGCAGTCTGGC
CAGTGTGCCGGGGCTGCACTGGACGTGTTTACGGAAGAGCCGCCACGGGACCGGGCCTTGGTGGACCATGAGAATG
TCATCAGCTGTCCCCACCTGGGTGCCAGCACCAAGGAGGCTCAGAGCCGCTGTGGGGAGGAAATTGCTGTTGAGTT
CGTGGACATGGTGAAGGGGAAATCTCTACGGGGGTTGTGAATGCCAGGCCCTT

Fig. 1S

AGCCAGATGGCTGAGAGCTGCAAGAAGAAGTCAGGATCATGATGGCTCAGTTTCCCACAGCGATGAATGGAGGGCC
AAATATGTGGGCTATTACATCTGAAGAACGTACTAAGCATGATAAACAGTTTGATAACCTCAAACCTTCAGGAGGT
TACATAACAGGTGATCAAGCCCGTACTTTTTCTACAGTCAGGTCTGCCGGCCCCGGTTTTAGCTGAAATATGGG
CCTTATCAGATCTGAACAAGGATGGGAAGATGGACCAGCAAGAGTTCTCTATAGCTATGAAACTCATCAAGTAAA
GTTGCAGGGCCAACAGCTGCCTGTAGTCCTCCCTCCTATCATGAAACAACCCCTATGTTCTCTCCACTAATCTCT
GCTCGTTTTGGGATGGGAAGCATGCCAATCTGTCCATTATCATCAGCCATTGCCTCCAGTTGCACCTATAGCAACAC
CCTTGCTCTTCTGCTACTTCAGGGACCAGTATTCTCCCCTAATGATGCCTGCTCCCCTAGTGCCTTCTGTTAGTAC
ATCCTCATTACCAAATGGAAGTCCAGTCTCATTAGCCTTTATCCATTCTTATTCTTCTTCAACATTGCCTCAT
GCATCATCTTACAGCCTGATGATGGGAGGATTTGGTGGTGCTAGTATCCAGAAGGCCAGTCTCTGATTGATTTAG
GATCTAGTAGCTCAACTTCCTCAACTGCTTCCCTCTCAGGGAACCTCACCTAAGACAGGGACCTCAGAGTGGGCAGT
TCCTCAGCCTTCAAGATTAAAGTATCGGCAAAAATTTAATAGTCTAGACAAAGGCATGAGCGGATACCTCTCAGGT
TTTCAAGCTAGAAATGCCCTTCTTCAGTCAAATCTCTCAAACCTCAGCTAGCTACTATTTGGACTCTGGCTGACA
TCGATGGTGACGGACAGTTGAAAGCTGAAGAATTTATTCTGGCGATGCACCTCACTGACATGGCCAAAGCTGGACA
GCCACTACCACTGACGTTGCCTCCCGAGCTTGTCCTCCATCTTTCAGAGGGGGAAAGCAAGTTGATTCTGTTAAT
GGAAGTCTGCCTTCATATCAGAAAACACAAGAAGAAGAGCCTCAGAAGAACTGCCAGTTACTTTTGAGGACAAAC
GGAAAGCCAACTATGAACGAGGAAACATGGAGCTGGAGAAGCGACGCCAAGTGTTGATGGAGCAGCAGCAGAGGGA
GGCTGAACGCAAAGCCCAGAAAGAGAAGGAAGAGTGGGAGCGGAAACAGAGAGAACTGCAAGAGCAAGAATGGAAG
AAGCAGCTGGAGTTGGAGAAACGCTTGGAGAAACAGAGAGAGCTGGAGAGACAGCGGGAGGAAGAGAGGAGAAAGG
AGATAGAAAGACGAGAGGCAGCAAAACAGGAGCTTGAGAGACAACGCCGTTTAGAATGGGAAAGACTCCGTGCGCA
GGAGCTGCTCAGTCAGAAGACCAGGGAACAAGAAGACATTGTCAGGCTGAGCTCCAGAAAGAAAAGTCTCCACCTG
GAACTGGAAGCAGTGAATGGAAAACATCAGCAGATCTCAGGCAGACTACAAGATGTCCAAATCAGAAAGCAAACAC
AAAAGACTGAGCTAGAAGTTTTGGATAAACAGTGTGACCTGGAAATTATGGAAATCAAACAACCTTCAACAAGAGCT
TAAGGAATATCAAAATAAGCTTATCTATCTGGTCCCTGAGAAGCAGCTATTAACGAAAGAATTAACAAATGCAG
CTCAGTAACACACCTGATTCAGGGATCAGTTTACTTCATAAAAAGTCATCAGAAAAGGAAGAATTATGCCAAAGAC
TTAAAGAACAATTAGATGCTCTTGAAAAAGAACTGCATCTAAGCTCTCAGAAATGGATTCAATTAACAATCAGCT
GAAGGAACTCAGAGAAAGCTATAATACACAGCAGTTAGCCCTTGAACAACCTTCATAAAATCAAACGTGACAAATTG
AAGGAAATCGAAAGAAAAAGATTAGAGCAAAAAAAAAAAAA

Fig. 2A

Title: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF OVARIAN CANCER

Inventors: Jennifer L. Mitcham et al. Ser No. 09/636,801

Docket No. 210121.462C4 Express Mail No. EV020613020US

ATGGCAGTGACATTCACCATCATGGGAACCACTTCCCTTTTCTTCAGGATTCTCTGTAGTGGAAGAGAGCACCCA
GTGTTGGGCTGAAAACATCTGAAAGTAGGGAGAAGAACCTAAAATAATCAGTATCTCAGAGGGCTCTAAGGTGCCA
AGAAGTCTCACTGGACATTTAAGTGCCAACAAAGGCATACTTTCGGAATCGCCAAGTCAAAACTTTCTAACTTCTG
TCTCTCTCAGAGACAAGTGAGACTCAAGAGTCTACTGCTTTAGTGGCAACTACAGAAAAGTGGTGTTACCCAGAAA
AACAGGAGCAATTAGAAATGGTTCCAATATTTCAAAGCTCCGCAACAGGATGTGCTTTCCTTTGCCCATTTAGGG
TTTCTTCTCTTTCCTTTCTCTTTATTAACCACTA

Fig. 2B

ATATCTAGAAGTCTGGAGTGAGCAAACAAGAGCAAGAAACAAAAAGAAGCCAAAAGCAGAAGGCTCCAATATGAAC
AAGATAAATCTATCTTCAAAGACATATTAGAAGTTGGGAAAATAATTCATGTGAAGTAGACAAGTGTGTTAAGAGT
GATAAGTAAAATGCACGTGGAGACAAGTGCATCCCCAGATCTCAGGGACCTCCCCCTGCCTGTCACCTGGGGAGTG
AGAGGACAGGATAGTGCATGTTCTTTGTCTCTGAATTTTTAGTTATATGTGCTGTAATGTTGCTCTGAGGAAGCCC
CTGGAAAGTCTATCCCAACATATCCACATCTTATATTCCACAAATTAAGCTGTAGTATGTACCCTAAGACGCTGCT
AATTGACTGCCACTTCGCAACTCAGGGGCGGCTGCATTTTTAGTAATGGGTCAAATGATTCACCTTTTTATGATGCTT
CCAAAGGTGCCTTGGCTTCTCTTCCCAACTGACAAATGCCAAAGTTGAGAAAAATGATCATAATTTTAGCATAAAC
AGAGCAGTCGGCGACACCGATTTTATAAATAAACTGAGCACCTTCTTTTTAAACAAACAAATGCGGGTTTATTTCT
CAGATGATGTTTCATCCGTGAATGGTCCAGGGAAGGACCTTTACCTTGACTATATGGCATTATGTCATCACAAGCT
CTGAGGCTTCTCCTTTCCATCCTGCGTGGACAGCTAAGACCTCAGTTTTCAATAGCATCTAGAGCAGTGGGACTCA
GCTGGGGTGATTTGCGCCCCCATCTCCGGGGGAATGTCTGAAGACAATTTTGTTACCTCAATGAGGGAGTGGAGGA
GGATACAGTGCTACTACCAACTAGTGGATAAAGGCCAGGGATGCTGCTCAACCTCCTACCATGTACAGGACGTCTC
CCCATTACAACCTACCCAATCCGAAGTGTCAACTGTGTCAGGACTAAGAAACCCTGGTTTTGAGTAGAAAAGGGCCT
GGAAAGAGGGGAGCCAACAAATCTGTCTGCTTCTCACATTAGTCATTGGCAAATAAGCATTCTGTCTCTTTGGCT
GCTGCCTCAGCACAGAGAGCCAGAACTCTATCGGGCACCAGGATAACATCTCTCAGTGAACAGAGTTGACAAGGCC
TATGGGAAATGCCTGATGGGATTATCTTCAGCTTGTTGAGCTTCTAAGTTTTCTTCCCTTCATTCTACCCTGCAAG
CCAAGTTCTGTAAGAGAAATGCCTGAGTTCTAGCTCAGGTTTTCTTACTCTGAATTTAGATCTCCAGACCCTTCT
GGCCACAATTCAAATTAAGGCAACAAACATATACCTTCCATGAAGCACACACAGACTTTTGAAAGCAAGGACAATG
ACTGCTTGAATTGAGGCCTTGAGGAATGAAGCTTTGAAGGAAAAGAATACTTTGTTTCCAGCCCCCTTCCCACACT
CTTCATGTGTTAACCCTGCCTTCTGGACCTTGGAGCCACGGTGACTGTATTACATGTTGTTATAGAAAAGTAT
TTTAGAGTTCTGATCGTTCAAGAGAATGATTAAATATACATTTCTA

Fig. 2C

| Probe 1 | Exp | Probe 2 | Gene/Element | Plate/Well | Probe 1 | S/B | A% | Probe 2 | S/B | A% |
|---------------------|-----|------------------------|----------------|-----------------|---------|------|----|---------|-----|----|
| 384A Ovary T (mets) | + | 272A Dendritic cells | 422A0608 (420) | 421G0196 (C:11) | 2393 | 13.7 | 50 | 1430 | 2.0 | 50 |
| 335A Ovary T | - | S7 Ovary N | 422D0626 (420) | 421G0196 (C:11) | 355 | 2.7 | 54 | 382 | 1.8 | 54 |
| 261A Ovary T | + | S10 Skeletal muscle N | 42230621 (420) | 421G0196 (C:11) | 1298 | 6.9 | 51 | 707 | 1.9 | 51 |
| 264A Ovary T | + | S2 Pancreas N | 422N0629 (420) | 421G0196 (C:11) | 9590 | 44.0 | 62 | 1180 | 2.3 | 62 |
| 386A Ovary T | - | S40 PBMC (activated) | 422J0605 (420) | 421G0196 (C:11) | 516 | 3.8 | 50 | 618 | 2.0 | 50 |
| 265A Ovary T | + | CT5 Heart N | 422O0624 (420) | 421G0196 (C:11) | 2305 | 14.8 | 53 | 489 | 2.2 | 53 |
| S25 Ovary T | - | CT4 Bone Marrow N | 422H0619 (420) | 421G0196 (C:11) | 531 | 3.5 | 53 | 743 | 2.0 | 53 |
| 383A Ovary T (mets) | + | I1 Colon N | 422B0609 (420) | 421G0196 (C:11) | 1842 | 10.8 | 39 | 671 | 2.0 | 39 |
| S22 Ovary T | - | CT9 Kidney N | 42290627 (420) | 421G0196 (C:11) | 453 | 3.3 | 68 | 857 | 3.2 | 68 |
| 9485 OT 1-P (SCID) | + | 9485 OT 5-P (SCID) | 422Y0602 (420) | 421G0196 (C:11) | 1882 | 12.1 | 57 | 594 | 2.3 | 57 |
| 262A Ovary T | + | 334A Large Intestine N | 422A0622 (420) | 421G0196 (C:11) | 1486 | 7.5 | 55 | 965 | 2.2 | 55 |
| S115 Ovary T (mets) | - | CT10 Small Intestine N | 422C0604 (420) | 421G0196 (C:11) | 509 | 3.4 | 51 | 573 | 2.0 | 51 |
| 288A Ovary T | + | CT12 Lung N | 422V0625 (420) | 421G0196 (C:11) | 700 | 4.5 | 54 | 651 | 2.1 | 54 |
| 201A Ovary T | - | S6 Stomach N | 422W0620 (420) | 421G0196 (C:11) | 625 | 4.6 | 46 | 1335 | 3.6 | 46 |
| S23 Ovary T | + | S56 Spinal Cord N | 422G0628 (420) | 421G0196 (C:11) | 3886 | 22.1 | 50 | 502 | 2.2 | 50 |
| 205A Ovary T | + | 270A Liver N | 422Q0606 (420) | 421G0196 (C:11) | 2251 | 14.7 | 46 | 1256 | 2.0 | 46 |
| 9334 Ovary T (SCID) | - | I2 Skin N | 422R0601 (420) | 421G0196 (C:11) | 552 | 3.4 | 72 | 1029 | 2.3 | 72 |
| 365A Ovary T | + | S91 Fetal tissue | 422X0607 (420) | 421G0196 (C:11) | 8126 | 35.8 | 50 | 1449 | 2.0 | 50 |
| 263A Ovary T | - | S73 Breast N | 422H0623 (420) | 421G0196 (C:11) | 439 | 3.2 | 61 | 1531 | 3.4 | 61 |
| 382A Ovary T | + | CT19 Brain N | 422Q0610 (420) | 421G0196 (C:11) | 387 | 3.2 | 50 | 1278 | 2.1 | 50 |
| 266A Ovary T | + | S27 Ovary N | 422S0603 (420) | 421G0196 (C:11) | 4242 | 22.1 | 58 | 883 | 2.0 | 58 |

Fig. 3

Title: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF OVARIAN CANCER

Inventors: Jennifer L. Mitcham et al. Ser. No. 09/636,801

Docket No. 210121.462C4 Express Mail No. EV020613020US

TCGAGCGGCCCGCCCGGGCAGGTCCTTCAGACTTGGACTGTGTCACACTGCCAGGCTTCAGGGCTCCAACTTGCAG
ACGGCCTGTTGTGGGACAGTCTCTGTAATCGCGAAAGCAACCATGGAAGACCTGGGGGAAAACACCATGGTTTTAT
CCACCCTGAGATCTTTGAACAACCTTCATCTCTCAGCGTGCGGAGGGAGGCTCTGGACTGGATATTTCTACCTCGGC
CGCGACCACGCT

Fig. 4

Title: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF OVARIAN CANCER

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Docket No. 210121.462C4 Express Mail No. EV020613020US

TAGCGYGGTCGCGGCCGAGGYCTGCTTYTCTGTCCAGCCCAGGGCCTGTGGGGTCAGGGCGGTGGGTGCAGATGGC
ATCCACTCCGGTGGCTTCCCCATCTTTCTCTGGCCTGAGCAAGGTCAGCCTGCAGCCAGAGTACAGAGGGCCAACA
CTGGTGTTCTTGAACAAGGGCCTTAGCAGGCCCTGAAGGRCCCTCTCTGTAGTGTTGAACTTCCTGGAGCCAGGCC
ACATGTTCTCCTCATACCGCAGGYTAGYGATGGTGAAGTTGAGGGTGAAATAGTATTMANGRAGATGGCTGGCARA
CCTGCCCCGGGCGGCCGCTCSAAATCC

Fig. 5

Title: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF OVARIAN CANCER

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Docket No. 210121.462C4 Express Mail No. EV020613020US

AGCGTGGTCGCGGCCGAGGTGTCCTTCAGGGTCTGCTTATGCCCTTGTTCAAGAACACCAGTGTCTCTGTA
CTCTGGTTGCAGACTGACCTTGCTCAGGCCTGAGAAGGATGGGGCAGCCACCAGAGTGGATGCTGTCTGCACCCAT
CGTCCTGACCCCAAAGCCCTGGACTGGACAGAGAGCGGCTGTACTGGAAGCTGAGCCAGCTGACCCACGGCATCA
CTGAGCTGGGCCCCTACACCCTGGACAGGGACAGTCTCTATGTCAATGGTTTCACCCATCGGAGCTCTGTACCCAC
CACCAGCACCGGGGTGGTCAGCGAGGAGCCATTCAACCTGCCCGGGCGGCCGCTCGA

Fig. 6

Fig. 7A

TTGGGGNTTTMGAGCGGCCGCCCGGGCAGGTACCGGGGTGGTCAGCGAGGAGCCATTACACTGAACTTCACCATC
AACAACTGCGGTATGAGGAGAACATGCAGCACCTGGCTCCAGGAAGTTCAACACCACGGAGAGGGTCCTTCAGG
GCCTGCTCAGGTCCCTGTTCAAGAGCACCAAGTGTGGCCCTCTGTACTCTGGCTGCAGACTGACTTTGCTCAGACT
TGAGAAACATGGGGCAGCCACTGGAGTGGACGCCATCTGCACCCTCCGCCTTGATCCCACTGGTCCTGGACTGGAC
AGAGAGCGGCTATACTGGGAGCTGAGCCAGTCCTCTGGCGGNGACNCCNCTT

Fig. 7B

AGCGTGGTCGCGGCCGAGGTCCAGTCGCAGCATGCTCTTTCTCCTGCCCCACTGGCACAGTGAGGAAGATCTCTGCT
GTCAGTGAGAAGGCTGTCATCCACTGAGATGGCAGTCAAAGTGCATTTAATACACCTAACGTATCGAACATCATA
GCTTGCCCCAGGTTATCTCATATGTGCTCAGAACACTTACAATAGCCTGCAGACCTGCCCCGGCGGCCGCTCGA

Fig. 7A and 7B

Title: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF OVARIAN CANCER

Inventors: Jennifer L. Mitcham et al. Ser. No. 09/636,801

Docket No. 210121.462C4 Express Mail No. EV020613020US

TGTGGTGTGAACTTCCTGGAGNCAGGGTGACCCATGTCCTCCCCATACTGCAGGTTGGTGATGGTGAAGTTGAGG
GTGAATGGTACCAGGAGAGGGCCAGCAGCCATAATTGTSGRGCKGSMGMSSGAGGMWGGWGTYYCWGAGGTTCYRA
RRTCCACTGTGGAGGTCCCAGGAGTGCTGGTGGTGGGCACAGAGSTCYGATGGGTGAAACCATTGACATAGAGACT
GTTCTGTCCAGGGTGTAGGGGCCAGCTCTTYRATGYCATTGGYCAGTTKGCTYAGCTCCCAGTACAGCCRCTCT
CKGYYGMWCCAGSGCTTTTGGGGTCAAGATGATGGATGCAGATGGCATCCACTCCAGTGGCTGCTCCATCCTTCT
CGGACCTGAGAGAGGTGAGTCTGCAGCCAGAGTACAGAGGGCCAACACTGGTGTCTTTGAATA

Fig. 8

Title: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF OVARIAN CANCER

Inventors: Jennifer L. Mitcham et al. Ser. No. 09/636,801

Docket No. 210121.462C4 Express Mail No. EV020613020US

TCGAGCGGCCGCGCCGGGCAGGTCAGGAAGCACATTGGTCTTAGAGCCACTGCCTCCTGGATTCCACCTGTGCTGCG
GACATCTCCAGGGAGTGCAGAAGGGAAGCAGGTCAAACCTGCTCAGATCAGTCAGACTGGCTGTTCTCAGTTCTCAC
CTGAGCAAGGTCAGTCTGCAGCCAGAGTACAGAGGGCCAACACTGGTGTTCCTGAACAAGGGCTTGAGCAGACCCT
GCAGAACCTCTTCCGTGGTGTGAACTTCCTGGAACAGGGTGTTCATGTTTTCTCATAATGCAAGGTTGG
TGATGG

Fig. 9

| Gene Name | Exp Name | Probe 1 | Probe 2 | GEM ID | Probe1 Value | Probe2 Value | Probe1 S/B | Probe1 A% | Probe2 S/B | Probe2 A% |
|---------------|--------------------------|---------|---------|----------------------|--------------|--------------|------------|-----------|------------|-----------|
| 42100188 (D3) | +7.0 205A Ovary T | P1 | P2 | 270A Liver N | 8620 | 1240 | 57.7 | 65 | 2.2 | 65 |
| 42100188 (D3) | +5.9 523 Ovary T | P1 | P2 | S56 Spinal Cord N | 5894 | 1002 | 35.3 | 89 | 3.9 | 89 |
| 42100188 (D3) | +5.7 385A Ovary T | P1 | P2 | S91 Fetal tissue | 12151 | 2121 | 54.3 | 73 | 2.8 | 73 |
| 42100188 (D3) | +5.1 426A Ovary T (met) | P1 | P2 | 415A Aorta N | 7487 | 1480 | 53.0 | 73 | 9.7 | 73 |
| 42100188 (D3) | +3.5 263A Ovary T | P1 | P2 | S73 Breast N | 7302 | 2116 | 39.2 | 84 | 4.5 | 84 |
| 42100188 (D3) | +3.3 383A Ovary T (met) | P1 | P2 | I1 Colon N | 3714 | 1113 | 20.4 | 83 | 2.6 | 83 |
| 42100188 (D3) | +3.0 933A Ovary T (SCID) | P1 | P2 | I2 Skin N | 2435 | 814 | 12.1 | 75 | 2.1 | 75 |
| 42100188 (D3) | +2.6 384A Ovary T (met) | P1 | P2 | 272A Dendritic cell | 4578 | 1754 | 25.0 | 69 | 2.3 | 69 |
| 42100188 (D3) | +2.2 264A Ovary T | P1 | P2 | S2 Pancreas N | 7904 | 3596 | 38.5 | 81 | 5.6 | 81 |
| 42100188 (D3) | +2.0 386A Ovary T | P1 | P2 | S40 PR MC (activat) | 2191 | 1081 | 14.0 | 90 | 2.9 | 90 |
| 42100188 (D3) | +2.0 5115 Ovary T (met) | P1 | P2 | CT10 Small intestine | 1979 | 971 | 10.4 | 80 | 2.7 | 80 |
| 42100188 (D3) | +2.0 265A Ovary T | P1 | P2 | CT5 Heart N | 1911 | 964 | 13.9 | 93 | 3.4 | 93 |
| 42100188 (D3) | +2.0 335A Ovary T | P1 | P2 | S7 Ovary N | 1660 | 817 | 9.8 | 100 | 3.0 | 100 |
| 42100188 (D3) | -1.9 428A Ovary T (met) | P1 | P2 | 243A Esophagus N | 1827 | 3480 | 13.4 | 97 | 9.5 | 97 |
| 42100188 (D3) | +1.6 261A Ovary T | P1 | P2 | S10 Skeletal muscle | 5914 | 3653 | 30.4 | 86 | 6.0 | 86 |
| 42100188 (D3) | +1.6 266A Ovary T | P1 | P2 | S27 Ovary N | 2039 | 1274 | 11.9 | 50 | 2.6 | 50 |
| 42100188 (D3) | +1.6 S22 Ovary T | P1 | P2 | CT9 Kidney N | 1736 | 1072 | 11.0 | 92 | 4.0 | 92 |
| 42100188 (D3) | +1.4 9485 OT 1-P (SCID) | P1 | P2 | 9485 OT 5-P (SCID) | 4204 | 3074 | 23.0 | 93 | 7.7 | 93 |
| 42100188 (D3) | +1.4 262A Ovary T | P1 | P2 | 334A Large Intestine | 3002 | 2101 | 16.6 | 89 | 4.0 | 89 |
| 42100188 (D3) | +1.3 S25 Ovary T | P1 | P2 | CT4 Bone Marrow | 1643 | 1297 | 9.6 | 90 | 3.1 | 90 |
| 42100188 (D3) | +1.2 429A Ovary T (met) | P1 | P2 | 364A Ovary N | 2521 | 2084 | 22.0 | 65 | 2.9 | 65 |
| 42100188 (D3) | +1.2 382A Ovary T | P1 | P2 | CT19 Brain N | 2072 | 1663 | 10.9 | 88 | 2.3 | 88 |
| 42100188 (D3) | +1.2 288A Ovary T | P1 | P2 | CT12 Lung N | 1840 | 1473 | 10.7 | 87 | 3.8 | 87 |
| 42100188 (D3) | +1.1 201A Ovary T | P1 | P2 | S6 Stomach N | 1329 | 1204 | 9.1 | 90 | 3.5 | 90 |

Fig. 10

| Gene Name | Bel Probe 1 Exp Name | P1 | P2 Name | Probe 2 | Gene ID | Probe1 Value | Probe2 Value | Probe1 S/B | Probe1 A% | Probe2 S/B | Probe2 A% |
|---------------|---------------------------|----|----------------------|----------|----------|--------------|--------------|------------|-----------|------------|-----------|
| 421B0181 (C3) | +18.8 385A Ovary T | Ⓢ | S91 Fetal tissue | 422X0607 | 422X0607 | 26711 | 1424 | 103.3 | 54 | 2.0 | 54 |
| 421B0181 (C3) | +11.5 523 Ovary T | Ⓢ | S56 Spinal Cord N | 422G0628 | 422G0628 | 13559 | 1179 | 65.3 | 68 | 3.9 | 68 |
| 421B0181 (C3) | +11.1 426A Ovary T (mets) | Ⓢ | 415A Aorta N | 422X0611 | 422X0611 | 14125 | 1273 | 67.3 | 61 | 5.6 | 61 |
| 421B0181 (C3) | +10.8 205A Ovary T | Ⓢ | 270A Liver N | 422Q0606 | 422Q0606 | 16121 | 1488 | 93.1 | 43 | 2.3 | 43 |
| 421B0181 (C3) | +5.1 263A Ovary T | Ⓢ | S73 Breast N | 422H0623 | 422H0623 | 11326 | 2235 | 58.2 | 68 | 4.4 | 68 |
| 421B0181 (C3) | +4.6 384A Ovary T (mets) | Ⓢ | 272A Dendritic cells | 422A0608 | 422A0608 | 6583 | 1424 | 24.5 | 40 | 2.1 | 40 |
| 421B0181 (C3) | +4.4 264A Ovary T | Ⓢ | S2 Pancreas N | 422N0629 | 422N0629 | 9865 | 2245 | 40.9 | 64 | 3.6 | 64 |
| 421B0181 (C3) | +4.4 429A Ovary T (mets) | Ⓢ | 364A Ovary N | 422I0614 | 422I0614 | 2803 | 638 | 22.6 | 60 | 7.4 | 60 |
| 421B0181 (C3) | +4.2 261A Ovary T | Ⓢ | S10 Skeletal muscle | 422Y0621 | 422Y0621 | 8271 | 1949 | 39.5 | 68 | 3.6 | 68 |
| 421B0181 (C3) | +3.8 5115 Ovary T (mets) | Ⓢ | CT10 Small intestine | 422C0604 | 422C0604 | 2281 | 607 | 11.6 | 60 | 2.1 | 60 |
| 421B0181 (C3) | +2.5 265A Ovary T | Ⓢ | CT5 Heart N | 422O0624 | 422O0624 | 3192 | 1293 | 19.2 | 68 | 4.0 | 68 |
| 421B0181 (C3) | -2.3 522 Ovary T | Ⓢ | CT9 Kidney N | 422N0627 | 422N0627 | 565 | 1276 | 3.6 | 70 | 3.9 | 70 |
| 421B0181 (C3) | +2.2 266A Ovary T | Ⓢ | S27 Ovary N | 422S0603 | 422S0603 | 2774 | 1260 | 14.3 | 46 | 2.7 | 46 |
| 421B0181 (C3) | +2.1 933A Ovary T (SCID) | Ⓢ | 12 Skin N | 422R0601 | 422R0601 | 1774 | 837 | 8.4 | 56 | 2.1 | 56 |
| 421B0181 (C3) | +1.9 9485 OT 1-P (SCID) | Ⓢ | 9485 OT 5-P (SCID) | 422Y0602 | 422Y0602 | 6967 | 3726 | 41.5 | 70 | 9.2 | 70 |
| 421B0181 (C3) | +1.6 382A Ovary T | Ⓢ | CT19 Brain N | 422Q0610 | 422Q0610 | 2313 | 1471 | 6.2 | 50 | 1.9 | 50 |
| 421B0181 (C3) | +1.6 288A Ovary T | Ⓢ | CT12 Lung N | 422V0625 | 422V0625 | 1657 | 1054 | 9.7 | 69 | 2.9 | 69 |
| 421B0181 (C3) | -1.5 525 Ovary T | Ⓢ | CT4 Bone Marrow N | 422H0619 | 422H0619 | 848 | 1243 | 4.5 | 65 | 2.7 | 65 |
| 421B0181 (C3) | +1.4 262A Ovary T | Ⓢ | 334A Large Intestine | 422A0622 | 422A0622 | 3171 | 2214 | 16.8 | 69 | 3.8 | 69 |
| 421B0181 (C3) | +1.2 386A Ovary T | Ⓢ | S40 PBMC (activated) | 422I0605 | 422I0605 | 630 | 544 | 4.2 | 53 | 1.9 | 53 |
| 421B0181 (C3) | -1.2 335A Ovary T | Ⓢ | S7 Ovary N | 422W0626 | 422W0626 | 592 | 730 | 3.7 | 75 | 2.6 | 75 |
| 421B0181 (C3) | -1.0 201A Ovary T | Ⓢ | S6 Stomach N | 422W0620 | 422W0620 | 1197 | 1237 | 7.8 | 65 | 3.5 | 65 |
| 421B0181 (C3) | -1.0 428A Ovary T (mets) | Ⓢ | 243A Esophagus N | 422A0612 | 422A0612 | 783 | 797 | 4.5 | 95 | 2.4 | 95 |
| 421B0181 (C3) | 383A Ovary T (mets) | Ⓢ | 11 Colon N | 422B0609 | 422B0609 | 3470 | 862 | 8.9 | 24 | 1.7 | 24 |

Fig. 11

| Gene Name | Bas. Probe 1 Exp Name | P1 | P2 Name | Probe 2 ID | GEM ID | Probe1 Value | Probe2 Value | Probe1 S/B | Probe2 S/B | Probe1 A% | Probe2 A% |
|---------------|--------------------------|---------------|----------------------|---------------|-----------|-----------------|-----------------|---------------|---------------|--------------|--------------|
| 42110182 (H7) | +16.7 426A Ovary T (met) | 42110182 (H7) | 415A Aorta N | 422X0611 | 422X0611 | 7706 | 462 | 46.3 | 3.5 | 75 | 75 |
| 42110182 (H7) | +10.7 205A Ovary T | 42110182 (H7) | 270A Liver N | 422Q0606 | 422Q0606 | 10171 | 950 | 61.2 | 1.8 | 41 | 41 |
| 42110182 (H7) | +9.9 385A Ovary T | 42110182 (H7) | S91 Fetal tissue | 422X0607 | 422X0607 | 14415 | 1459 | 62.1 | 2.2 | 48 | 48 |
| 42110182 (H7) | +8.8 S23 Ovary T | 42110182 (H7) | S56 Spinal Cord N | 422H0628 | 422H0628 | 7781 | 880 | 47.3 | 3.4 | 73 | 73 |
| 42110182 (H7) | +6.4 383A Ovary T (met) | 42110182 (H7) | 11 Colon N | 422B0609 | 422B0609 | 4807 | 748 | 27.6 | 2.2 | 47 | 47 |
| 42110182 (H7) | +5.1 263A Ovary T | 42110182 (H7) | S73 Breast N | 422H0623 | 422H0623 | 9815 | 1909 | 57.1 | 4.2 | 74 | 74 |
| 42110182 (H7) | +4.9 429A Ovary T (met) | 42110182 (H7) | 364A Ovary N | 422I0614 | 422I0614 | 2661 | 543 | 20.3 | 6.7 | 61 | 61 |
| 42110182 (H7) | +3.5 264A Ovary T | 42110182 (H7) | S2 Pancreas N | 422N0629 | 422N0629 | 7934 | 2274 | 38.8 | 3.9 | 71 | 71 |
| 42110182 (H7) | -2.9 S25 Ovary T | 42110182 (H7) | CT4 Bone Marrow | 422H0619 | 422H0619 | 480 | 1375 | 3.5 | 3.0 | 80 | 80 |
| 42110182 (H7) | +2.8 261A Ovary T | 42110182 (H7) | S10 Skeletal muscle | 422Q0621 | 422Q0621 | 8993 | 3245 | 34.6 | 5.1 | 69 | 69 |
| 42110182 (H7) | +2.5 S115 Ovary T (met) | 42110182 (H7) | CT10 Small intestine | 422C0604 | 422C0604 | 1864 | 738 | 8.1 | 2.2 | 67 | 67 |
| 42110182 (H7) | -2.3 9334 Ovary T (SCII) | 42110182 (H7) | 12 Skin N | 422R0601 | 422R0601 | 2552 | 1113 | 12.7 | 2.6 | 41 | 41 |
| 42110182 (H7) | -2.3 S22 Ovary T | 42110182 (H7) | CT19 Kidney N | 422N0627 | 422N0627 | 386 | 889 | 3.2 | 3.4 | 69 | 69 |
| 42110182 (H7) | +2.2 384A Ovary T (met) | 42110182 (H7) | 272A Dendritic cell | 422A0608 | 422A0608 | 3516 | 1567 | 18.7 | 2.2 | 55 | 55 |
| 42110182 (H7) | -2.2 382A Ovary T | 42110182 (H7) | CT19 Brain N | 422Q0610 | 422Q0610 | 608 | 1320 | 4.2 | 2.3 | 60 | 60 |
| 42110182 (H7) | +1.9 265A Ovary T | 42110182 (H7) | CT5 Heart N | 422O0624 | 422O0624 | 2063 | 1080 | 13.6 | 3.5 | 87 | 87 |
| 42110182 (H7) | +1.8 266A Ovary T | 42110182 (H7) | S27 Ovary N | 422S0603 | 422S0603 | 1550 | 847 | 7.0 | 2.1 | 58 | 58 |
| 42110182 (H7) | +1.5 262A Ovary T | 42110182 (H7) | 334A Large Intestine | 422A0622 | 422A0622 | 2559 | 1651 | 13.2 | 3.2 | 73 | 73 |
| 42110182 (H7) | -1.4 386A Ovary T | 42110182 (H7) | S40 PB MC (activa) | 422I0605 | 422I0605 | 534 | 738 | 3.9 | 2.2 | 62 | 62 |
| 42110182 (H7) | -1.3 288A Ovary T | 42110182 (H7) | CT12 Lung N | 422V0625 | 422V0625 | 893 | 1120 | 5.3 | 3.1 | 66 | 66 |
| 42110182 (H7) | -1.3 335A Ovary T | 42110182 (H7) | S7 Ovary N | 422T0626 | 422T0626 | 440 | 567 | 3.3 | 2.2 | 60 | 60 |
| 42110182 (H7) | +1.2 9485 OT 1-P (SCID) | 42110182 (H7) | 9485 OT 5-P (SCID) | 422Y0602 | 422Y0602 | 4188 | 3529 | 21.6 | 9.5 | 66 | 66 |
| 42110182 (H7) | +1.1 428A Ovary T (met) | 42110182 (H7) | 243A Esophagus N | 422A0612 | 422A0612 | 725 | 689 | 6.2 | 2.8 | 65 | 65 |
| 42110182 (H7) | -1.0 201A Ovary T | 42110182 (H7) | S6 Stomach N | 422N0620 | 422N0620 | 1008 | 1018 | 7.4 | 3.2 | 62 | 62 |

Fig. 12

| Gene Name | Bal Probe 1 Exp Name | P1 | P2 Name | Probe 2 ID | GEM ID | Probe1 Value | Probe2 Value | S/B | A% | Probe1 S/B | A% | Probe2 S/B | A% |
|---------------|--------------------------|---------------|----------------------|---------------|-----------|-----------------|-----------------|-----|-----|---------------|-----|---------------|----|
| | | | | | | | | | | | | | |
| 421V0189 (D1) | +33.2 426A Ovary T (met) | 421V0189 (D1) | 415A Aorta N | 422X0611 | 8072 | 243 | 55.2 | 67 | 2.4 | 67 | 2.4 | 67 | 67 |
| 421V0189 (D1) | +13.7 523 Ovary T | 421V0189 (D1) | S36 Spinal Cord N | 422Q0628 | 7367 | 537 | 42.6 | 69 | 2.5 | 69 | 2.5 | 69 | 69 |
| 421V0189 (D1) | +12.6 429A Ovary T (met) | 421V0189 (D1) | S36A Ovary N | 422I0614 | 2850 | 227 | 21.7 | 64 | 3.5 | 64 | 3.5 | 64 | 64 |
| 421V0189 (D1) | +8.0 385A Ovary T | 421V0189 (D1) | S91 Fetal tissue | 422X0607 | 11711 | 1469 | 54.0 | 58 | 2.2 | 58 | 2.2 | 58 | 58 |
| 421V0189 (D1) | +7.3 263A Ovary T | 421V0189 (D1) | S73 Breast N | 422H0623 | 6949 | 952 | 37.8 | 69 | 2.6 | 69 | 2.6 | 69 | 69 |
| 421V0189 (D1) | -5.8 525 Ovary T | 421V0189 (D1) | CT4 Bone Marrow | 422H0619 | 208 | 1210 | 2.1 | 44 | 2.9 | 44 | 2.9 | 44 | 44 |
| 421V0189 (D1) | +5.0 205A Ovary T | 421V0189 (D1) | 270A Liver N | 422Q0606 | 8676 | 1937 | 52.3 | 57 | 2.6 | 57 | 2.6 | 57 | 57 |
| 421V0189 (D1) | +4.5 383A Ovary T (met) | 421V0189 (D1) | 11 Colon N | 422B0609 | 3149 | 707 | 17.4 | 57 | 2.0 | 57 | 2.0 | 57 | 57 |
| 421V0189 (D1) | +4.4 261A Ovary T | 421V0189 (D1) | S10 Skeletal muscle | 422J0621 | 6332 | 1443 | 29.1 | 77 | 2.9 | 77 | 2.9 | 77 | 77 |
| 421V0189 (D1) | +4.2 264A Ovary T | 421V0189 (D1) | S2 Pancreas N | 422N0629 | 7612 | 1809 | 38.1 | 79 | 3.3 | 79 | 3.3 | 79 | 79 |
| 421V0189 (D1) | -3.2 382A Ovary T | 421V0189 (D1) | CT19 Brain N | 422Q0610 | 468 | 1508 | 3.4 | 60 | 2.3 | 60 | 2.3 | 60 | 60 |
| 421V0189 (D1) | +2.9 9334 Ovary T (SCID) | 421V0189 (D1) | 12 Skin N | 422R0601 | 2500 | 860 | 12.3 | 51 | 2.1 | 51 | 2.1 | 51 | 51 |
| 421V0189 (D1) | +2.5 5115 Ovary T (met) | 421V0189 (D1) | CT10 Small intestine | 422C0604 | 1424 | 569 | 6.7 | 61 | 2.1 | 61 | 2.1 | 61 | 61 |
| 421V0189 (D1) | +2.4 265A Ovary T | 421V0189 (D1) | CT5 Heart N | 422Q0624 | 1742 | 723 | 11.8 | 70 | 2.8 | 70 | 2.8 | 70 | 70 |
| 421V0189 (D1) | +2.3 384A Ovary T (met) | 421V0189 (D1) | 272A Dendritic cell | 42240608 | 3083 | 1342 | 17.0 | 62 | 2.0 | 62 | 2.0 | 62 | 62 |
| 421V0189 (D1) | +1.9 266A Ovary T | 421V0189 (D1) | S27 Ovary N | 42250603 | 1370 | 732 | 8.0 | 47 | 2.0 | 47 | 2.0 | 47 | 47 |
| 421V0189 (D1) | -1.9 386A Ovary T | 421V0189 (D1) | S40 PBMC (activated) | 422J0605 | 307 | 580 | 2.6 | 41 | 2.0 | 41 | 2.0 | 41 | 41 |
| 421V0189 (D1) | +1.7 262A Ovary T | 421V0189 (D1) | 334A Large Intestine | 422A0622 | 2097 | 1202 | 11.2 | 86 | 2.7 | 86 | 2.7 | 86 | 86 |
| 421V0189 (D1) | -1.3 335A Ovary T | 421V0189 (D1) | S7 Ovary N | 42220626 | 373 | 470 | 2.9 | 47 | 2.0 | 47 | 2.0 | 47 | 47 |
| 421V0189 (D1) | -1.1 288A Ovary T | 421V0189 (D1) | CT12 Lung N | 422V0625 | 969 | 1094 | 5.6 | 72 | 2.9 | 72 | 2.9 | 72 | 72 |
| 421V0189 (D1) | +1.1 201A Ovary T | 421V0189 (D1) | S6 Stomach N | 422W0620 | 750 | 672 | 5.6 | 62 | 2.4 | 62 | 2.4 | 62 | 62 |
| 421V0189 (D1) | +1.1 428A Ovary T (met) | 421V0189 (D1) | 243A Esophagus N | 42240612 | 498 | 446 | 4.2 | 73 | 2.1 | 73 | 2.1 | 73 | 73 |
| 421V0189 (D1) | -1.0 9485 OT 1-P (SCID) | 421V0189 (D1) | 9485 OT 5-P (SCID) | 422Y0602 | 3117 | 3174 | 16.7 | 91 | 8.2 | 91 | 8.2 | 91 | 91 |
| 421V0189 (D1) | S22 Ovary T | 421V0189 (D1) | CT9 Kidney N | 42290627 | 224 | 409 | 2.3 | 48 | 2.3 | 48 | 2.3 | 48 | 48 |

Fig. 13

| Gene Name | Bel Probe 1 Exp Name | P1 | P2 Name | Probe 2 ID | GEM ID | Probe1 Value | Probe2 Value | Probe1 S/B | Probe1 A% | Probe2 S/B | Probe2 A% |
|----------------|--------------------------|----|----------------------|---------------|-----------|-----------------|-----------------|---------------|--------------|---------------|--------------|
| 421H0187 (E11) | +20.2 426A Ovary T (met) | + | 415A Aorta N | 422X0611 | 5441 | 270 | 36.3 | 50 | 2.3 | 50 | 50 |
| 421H0187 (E11) | +10.0 S23 Ovary T | + | S56 Spinal Cord N | 422C0628 | 5318 | 533 | 27.1 | 56 | 2.3 | 56 | 56 |
| 421H0187 (E11) | +8.3 429A Ovary T (met) | + | 364A Ovary N | 422I0614 | 1252 | 130 | 10.1 | 58 | 2.5 | 58 | 58 |
| 421H0187 (E11) | +5.7 385A Ovary T | + | S91 Fetal tissue | 422X0607 | 9507 | 1668 | 35.8 | 45 | 2.1 | 45 | 45 |
| 421H0187 (E11) | +4.4 205A Ovary T | + | 270A Liver N | 422Q0606 | 5456 | 1235 | 31.1 | 50 | 2.0 | 50 | 50 |
| 421H0187 (E11) | +4.2 265A Ovary T | + | CTS Heart N | 422O0624 | 1834 | 438 | 11.9 | 48 | 2.0 | 48 | 48 |
| 421H0187 (E11) | -4.1 382A Ovary T | + | CT19 Brain N | 422Q0610 | 309 | 1259 | 2.6 | 48 | 2.0 | 48 | 48 |
| 421H0187 (E11) | +3.6 261A Ovary T | + | S10 Skeletal muscle | 422J0621 | 3733 | 1036 | 17.7 | 55 | 2.3 | 55 | 55 |
| 421H0187 (E11) | +3.4 263A Ovary T | + | S73 Breast N | 422H0623 | 4163 | 1239 | 23.0 | 62 | 3.0 | 62 | 62 |
| 421H0187 (E11) | +2.5 S115 Ovary T (met) | + | CT10 Small intestine | 422C0604 | 1565 | 627 | 8.8 | 47 | 2.1 | 47 | 47 |
| 421H0187 (E11) | +2.1 264A Ovary T | + | S2 Pancreas N | 422N0629 | 3455 | 1630 | 14.9 | 60 | 3.0 | 60 | 60 |
| 421H0187 (E11) | +2.1 384A Ovary T (met) | + | 272A Dendritic cell | 42240608 | 2667 | 1270 | 13.4 | 44 | 1.9 | 44 | 44 |
| 421H0187 (E11) | -2.1 S22 Ovary T | + | CT9 Kidney N | 42290627 | 291 | 605 | 2.4 | 51 | 2.5 | 51 | 51 |
| 421H0187 (E11) | -1.7 386A Ovary T | + | S40 PBMC (activated) | 422J0605 | 410 | 687 | 3.2 | 47 | 2.0 | 47 | 47 |
| 421H0187 (E11) | +1.6 933A Ovary T (SCII) | + | 12 Skin N | 422R0601 | 1622 | 984 | 7.9 | 44 | 2.2 | 44 | 44 |
| 421H0187 (E11) | +1.5 262A Ovary T | + | 334A Large Intestine | 422A0622 | 1892 | 1245 | 10.1 | 50 | 2.6 | 50 | 50 |
| 421H0187 (E11) | -1.5 288A Ovary T | + | CT12 Lung N | 422V0625 | 604 | 908 | 4.1 | 62 | 2.6 | 62 | 62 |
| 421H0187 (E11) | -1.4 428A Ovary T (met) | + | 243A Esophagus | 42240612 | 236 | 325 | 2.7 | 78 | 1.9 | 78 | 78 |
| 421H0187 (E11) | -1.3 335A Ovary T | + | S7 Ovary N | 42220626 | 382 | 501 | 2.9 | 58 | 2.0 | 58 | 58 |
| 421H0187 (E11) | -1.2 201A Ovary T | + | S6 Stomach N | 422W0620 | 558 | 677 | 4.2 | 58 | 2.3 | 58 | 58 |
| 421H0187 (E11) | +1.0 9485 OT 1-P (SCID) | + | 9485 OT 5-P (SCID) | 422Y0602 | 2582 | 2493 | 15.1 | 57 | 6.3 | 57 | 57 |
| 421H0187 (E11) | 383A Ovary T (met) | + | 11 Colon N | 422B0609 | 2261 | 502 | 12.5 | 38 | 1.7 | 38 | 38 |
| 421H0187 (E11) | 266A Ovary T | + | S27 Ovary N | 42250603 | 1739 | 965 | 9.7 | 36 | 2.2 | 36 | 36 |
| 421H0187 (E11) | S25 Ovary T | + | CT4 Bone Marrow | 422H0619 | 283 | 845 | 2.2 | 44 | 2.2 | 44 | 44 |

Fig. 14

11721-1

ACGGTTTCAATGGACACTTTTATTGTTTACTTAATGGATCATCAATTTTGTCTCACTACCTACAAATGGAATTTCA
TCTTGTTCATGCTGAGTAGTGAAACAGTGACAAAGCTAATCATAATAACCTACATCAAAAGAGAACTAAGCTAA
CACTGCTCACTTTCTTTTAAACAGGCAAAATATAATATATGCACTCTAXAATGCACAATGGTTTAGTCACTAAAA
AATTCAAATGGGATCTTGAAGAATGTATGCAAATCCAGGGTGCAGTGAAGATGAGCTGAGATGCTGTGCAACTGTT
TAAGGGTTCCTGGCACTGCATCTCTTGGCCACTAGCTGAATCTTGACATGGAAGGTTTTAGCTAATGCCAAGTGGA
GATGCAGAAAATGCTAAGTTGACTTAGGGGCTGTGCACAGGAATAAAAGGCAGGAAAGTACTAAATATTGCTGAG
AGCATCCACCCAGGAAGGACTTTACCTTCAGGAGCTCCAACTGGCACCACCCCACTGCTCACATGGCTGACT
TTATCCTCCGTGTTCCATTTGGCACAGCAAGTGGCAGT

11721-2

AAGGCTGGTGGGTTTTTATCCTGCTGGAGAACCTCCGCTTTCATGTGGAGGAAGAAGGGAAGGGAAAAGATGCTT
CTGGGAACAAGGTTAAAGCCGAGCCAGCCAAAATAGAAGCTTTCGAGCTTCACTTTCCAAGCTAGGGGATGTCTA
TGTCATGATGCTTTTGGCACTGCTCACAGAGCCACAGCTCCATGGTAGGAGTCAATCTGCCACAGAAGGCTGGT
GGGTTTTTGTGAAGAAGGAGCTGAATACTTTGCAAAGGCCTTGAGAGCCAGAGCGACCCTTCCTGGCCATCC
TGGGCGGAGCTAAAGTTGCAGACAAGATCCAGCTCATCAATAATATGCTGGACAAAGTCAATGAGATGATTATTGG
TGGTGAATGGCTTTTACCTTCCTTAAGGTGCTCAACAACATGGAGATTGGCACTTCTCTGTTTGATGAAGAGGGA
GCCAAGATTGTCAAAGACCTAATGTCCAAAGCTGAGAAGAATGGTGTGAAGATTACCTTGCTGTTGACTTTGTCA
CTGCTGACAAGTTTGATGA

11724-1

TTTGTTCTTACATTTTTCTAAAGAGTTACTTAAATCAGTCAACTGGTCTTTGAGACTCTTAAGTTCTGATTCCAA
CTTAGCTAATTCATTCTGAGAACTGTGGTATAGGTGGCGTGTCTCTTCTAGCTGGGACAAAAGTTCTTTGTTTTCC
CCCTGTAGAGTATCACAGACCTTCTGCTGAAGCTGGACCTCTGTCTGGGCCCTTGACTCCCAATCTGCTTGTCTAT
GTTCAAGCCTGGAAATGTTAATCTTTAATCTTCCATATGGATGGACATCTGTCTAAGTTGATCCTTTAGAACACT
GCAATTATCTTCTTTGAGTCTAATTTCTTCTTTGCTTTGAATCGCATCACTAACTTCTCTCCCATTTCTTA
GCTTCATCTATCACCTGTACGATCATCTGGAGGGAAGACATGCTCTTAGTAAAGGCTGCAAGCTGGGTACAG
TACTGTCCAAGTTTTCTGAAGTTGCTGAACCTTCTTGTCTTTCTTGTTCAAAGTAACCTGAATCTCTCCAATTGT
CTCTTCCAAGTGGACTTTTTCTCTGCGCAAAGCATCCAG

11724-2

TCATTGCCTGTGATGGCATCTGGAATGTGATGAGCAGCCAGGAAGTTGTAGATTTCAATCAATCAAAGGATTTCAGC
ATGTGGTGGAAAGCTGTGAGGCAAGAGAAACAAGAACTGTATGGCAAGTTAAGAAGCACAGAGGCAAACAAGAAGGA
GACAGAAAAGCAGTTGCAGGAAGCTGAGCAAGAAATGGAGGAAATGAAAGAAAAGATGAGAAAAGTTTGCTAAATCT
AAACAGCAGAAAATCCTAGAGCTGGAAGAAGAGAATGACCGGCTTAGGGCAGAGGTGCACCCTGCAGGAGATACAG
CTAAAGAGTGTATGGAACACTTCTTTCTTCCAATGCCAGCATGAAGGAAGAACTTGAAAGGGTCAAATGGAGTA
TGAAACCTTTCTAAGAAGTTTCAGTCTTTAATGTCTGAGAAAGACTCTCTAAGTGAAGAGGTTCAAGATTTAAAG
CATCAGATAGAAGGTAATGTATCTAAACAAGCTAACCTAGAGGCCACCGAGAAACATGATAACCAAACGAATGTCA
CTGAAGAGGGAACACAGTCTATACCAGGT

Fig. 15A

AAGCCAATAATCACCATTATTACTTAATATATGCCAACCACTGTACTTGGCAGTTCACAAATTCTCACCGTTACA
ACAACCCCATGAGGTATTTATTCCCATTCTATAGATAGGGAAACCACAGCTCAAGTAAGTTAGGAACTGAGCCAA
GTATACACAGAATACGAAGTGGCAAACTAGAAGGAAAGACTGACACTGCTATCTGCTGGCCTCCAGTGTCTTGGC
TCTTTTACACGGGtTCAATGTCTCCAGCGCTGCTGCTGCTGCTGCATTACCATGCCCTCATTGTTTTCTTCTC
TGGTGTTCAACTGCATCCTTCAAAGAATCTAACTCATTCCAGAGACCACTTATTTCTTCTCTCTTCTGAAATTA
CTTTTAATAATTCTTCATGAGGGGGGAAAAGAAGATGCCTGTTGGTAGTTTTGTTGTTTAAGCTGCTCAATTTGGGA
CTTAAACAATTTGTTTTCATCTTGTAATCCTGTAACAGCTGTGTTTGCTAGAAAGATCACTCTCCCTCTCTTTT
AGCATGGCTTCTAACCTCTTCAATTCATTTTCTTTTCTTCAACACAATCTCAAGTTCTTCAAACGTGATGCAG
AAGAGGCCTCTTCAAGTTATGTTGTGCTACTTCCTGAACATGTGCTTTTAAAGATTCATTTTCTTCTTGAAGATC
CTGTAACCACTTCCCTGTATTGGCTAGGTCTTTCTCTTTCTCTTCCAAAACAGCCTTCATGGTATTCATCTGTTCC
TCTTTTCTTTTAATAAGTTCAGGAGCTTCAGAAC

CAAGCTTTTTTTTTTTTTTAAAAAGTGTTAGCATTAAATGTTTTATTGTACGCAGATGGCAACTGGGTTTATGTC
TTCATATTTTATATTTTGTAAATTAATAAATTACAAGTTTTAAATAGCCAATGGCTGGTTATATTTTCAGAAAA
CATGATTAGACTAATTCATTAATGGTGGCTTCAAGCTTTTCCTTATTGGCTCCAGAAAAATTCACCCACCTTTTGTCT
CCTTCTTAAAAAACTGGAATGTTGGCATGCATTTGACTTCACACTCTGAAGCAACATCCTGACAGTCATCCACATC
TACTTCAAGGAATATCACGTTGGAATACTTTTCAGAGAGGGAATGAAAGAAAGGCTTGATCATTTTGCAAGGCCCA
CACCACGTGGCTGAGAAGTCAACTACTACAAGTTTATCACCTGCAGCGTCCAAGGCTTCCTGAAAAGCAGTCTTGC
TCTCGATCTGCTTACCATCTTGGCTGCTGGAGTCTGACGAGCGGCTGTAAGGACCGATGGAAATGGATCCAAAGC
ACCAAACAGAGCTTCAAGACTCGCTGCTTGGCTTGAATTCGGATCCGATATCGCCATGGCT

AAGTGTTAGCATTAAATGTTTATTGTACGCAGATGGCAACTGGGTTTATGTCTTCATATTTTATATTTTTGTAA
TTAAAAAATTMCAAGTTTTAAATAGCCAATGGCTGGTTATATTTTCAGAAAACATGATTAGACTAATTCATTAAT
GGTGGCTTCAAGCTTTTCTTATTGGCTCCAGAAAATTCACCCACCTTTTGTCCCTTCTTAAAAAAGTGAATGTT
GGCATGCATTTGACTTCACACTCTGAAGCAACATCCTGACAGTCATCCACATCTACTTCAAGGAATATCACGTTGG
AATACTTTTCAGAGAGGGAATGAAAGAAAGGCTTGATCATTTTGCAAGGCCACACCACGTGGCTGAGAAGTCAAC
TACTACAAGTTTATCACCTGCAGCGTCCAAGGCTTCTGAAAAGCAGTCTTGCTCTCGATCTGCTTCACCATCTTG
GCTGCTGGAGTCTGACGAGCGGCTGTAAGGACCGATGGAAATGGATCCAAAGCACCAAACAGAGCTTCAAGACTCG
CTGCTTGGCATGAATTCGGATCCGA

Fig. 15B

11728.1.40.19.19

TACAAACTTTATTGAAACGCACACGCGCACACACACAAACACCCCTGTGGATAGGGAAAAGCACCTGGCCACAGGG
TCCACTGAAACGGGGAGGGGATGGCAGCTTGTAATGTGGCTTTTGCCACAACCCCTTCTGACAGGGAAGGCCTTA
GATTGAGGCCCCACCTCCCATGGTGATGGGGAGCTCAGAATGGGGTCCAGGGAGAATTTGGTTAGGGGGAGGTGCT
AGGGAGGCATGAGCAGAGGGGCACCCCTCCGAGTGGGGTCCCGAGGGCTGCAGAGTCTTCAGTACTGTCCCTCACAGC
AGCTGTCTCAAGGCTGGGTCCCTCAAAGGGGCGTCCAGCGCGGGGCTCCCTGCGCAAACACTTGGTACCCCTGG
CTGCGCAGCGGAAGCCAGCAGGACAGCAGTGGCGCCGATCAGCACAACAGACGCCCTGGCGGTAGGGACAGCAGGC
CCAGCCCTGTGCGTTGTCTCGGCAGCAGGTCTGGTTATCATGGCAGAAGTGTCTTCCACACTTCACGTCCTTCA
CACCCACGTGAXGGCTACXGGCCAGGAAG

11728.2.40.19.19

CCCGTGGGTGCCATCCACGGAGTTGTTACCTGATCTTTGGAAGCAGGATCGCCCGTCTGCACTGCAGTGGAAGCCC
CGTGGGCAGCAGTGATGGCCATCCCCGCATGCCACGGCCTCTGGGAAGGGGCAGCAACTGGAAGTCCCTGAGACGG
TAAAGATGCAGGAGTGGCCGGCAGAGCAGTGGGCATCAACCTGGCAGGGGCCACCCAGATGCCTGCTCAGTGTTGT
GGGCCATTTGTCCAGAAGGGGACGGCAGCAGCTGTAGCTGGCTCCTCCGGGGTCCAGGCAGCAGGCCACAGGGCAG
AACTGACCATCTGGGCACCGCGTTCCAGCCACCAGCCCTGCTGTAAAGGCCACCCAGCTCACCAGGGTCCACATGG
TCTGCCTGCGTCCGACTCCGCGGTCTTGGGCCCTGATGGTTCTACCTGCTGTGAGCTGCCAGTGGGAAGTATGG
CTGCTGCCAATGCCAACGCCACCTGCTGCTCCGATCACCTGCACTGCTGCCCCAAGACACTGTGTGTGACCTGAT
CCAGAGTAAGTGCCTCTCCAAGGAGAACG

11730-1

GAATCACCTTTCTGGTTTAGCTAGTACTTTGTACAGAACAAATGAGGTTTCCCACAGCGGAGTCTCCCTGGGCTCTG
TTTGGCTCTCGGTAAGGCAGGCCTACACCTTTTCTCTCTCTATGGAGAGGGGAATATGCATTAAGGTGAAAAGT
CACCTTCCAAAAGTGAGAAAAGGGATTGATTGCTGCTTCAGGACTGTGGAATTATTTGGAATGTTTTACAAATGGT
TGCTACAAAACAACAAAAAAGGTAATTACAAAATGTGTACATCACAACATGCTTTTTAAAGACATTATGCATTGTG
CTCACATTCCCTTAAATGTTGTTTCCAAAGGTGCTCAGCCTCTAGCCCAGCTGGATTCTCCGGGAAGAGGCAGAGA
CAGTTTGGCGAAAAAGACACAGGGAAGGAGGGGGTGGTGAAAGGAGAAAGCAGCCTTCCAGTTAAAGATCAGCCCT
CAGTTAAAGGTCAGCTTCCCGCAXGCTGGCCTCAXGCGGAGTCTGGGTGAGAGGGAGGAGCAGCAGCAGGGTGGGA
CTGGGGCGT

11730-2

AACCGGAGCGCGAGCAGTAGCTGGGTGGGCACCATGGCTGGGATCACCACCATCGAGGCGGTGAAGCGCAAGATCC
AGGTTCTGCAGCAGCAGGCAGATGATGCAGAGGAGCGAGCTGAGCGCCTCCAGCGAGAAGTTGAGGGAGAAAGGCG
GGCCCGGGAACAGGCTGAGGCTGAGGTGGCCTCCTTGAACCGTAGGATCCAGCTGGTTGAAGAAGAGCTGGACCGT
GCTCAGGAGCGCCTGGCCACTGCCCTGCAAAAGCTGGAAGAAGCTGAAAAAGCTGCTGATGAGAGTGAGAGAGGTA
TGAAGGTTATTGAAAACCGGGCTTAAAAGATGAAGAAAAGATGGAACCTCCAGGAAATCCAACTCAAAGAAGCTAA
GCACATTGCAGAAGAGGCAGATAGGAAGTATGAAGAGGTGGCTCGTAAGTTGGTGATCATTGAAGGAGACTTGGAA
CGCACAGAGGAACGAGCTGAGCTGGCAGAGTCCCGTTGCCGAGAGATGGATGAGCAGATTAGACTGATGGACCAGA
ACCTGAAGTGTCTGAGTGC

Fig. 15C

11732.1contig

GAGAACTTGGCCTTTATTGTGGGCCCAGGAGGGCACAAAGGTCAGGAGGCCCAAGGGAGGGATCTGGTTTTCTGGA
TAGCCAGGTCATAGCATGGGTATCAGTAGGAATCCGCTGTAGCTGCACAGGCCTCACTTGCTGCAGTTCGGGGGAG
AACACCTGCACTGCATGGCGTTGATGACCTCGTGGTACACGACAGAGCCATTGGTGCAGTGAAGGGCACGCGCAT
GGGCTCCGTCCTCGAGGGCAGGCAGCAGGAGCATTGCTCCTGCACATCCTCGATGTCAATGGAGTACACAGCTTTG
CTGGCACACTTTCCCTGGCAGTAATGAATGTCCACTTCCTCTTGGGACTTACAATCTCCCACTTTGATGTACTGCA
CCTTGGCTGTGATGTCTTTGCAATCAGGCTCCTCACATGTGTACAGCAGGTGCCTGGAATTTTACGATTTTGCC
TCCTTCAGCCAGACACTTGTGTTTCATCAAATGGTGGGCAGCCCGTGACCCTCTTCTCCAGATGTACTCTCCTCT

11732.2contig

GCCTGGACCTTGCCGGATCAGTGCCACACAGTGACTTGCTTGGCAAATGGCCAGACCTTGCTGCAGAGTCATCGTG
TCAATTGTGACCATGGACCCCGGCCTTCATGTGCCAACAGCCAGTCTCCTGTTCCGGGTGGAGGAGACGTGTGGCTG
CCGCTGGACCTGCCCTTGTGTGTGCACGGGCAGTTCCTCCTGGCACATCGTCACCTTCGATGGGCAGAATTTCAAG
CTTACTGGTAGCTGCTCCTATGTCATCTTTCAAACAAGGAGCAGGACCTGGAAGTGCTCCTCCACAATGGGGCT
GCAGCCCCGGGGCAAACAAGCCTGCATGAAGTCCATTGAGATTAAGCATGCTGGCGTCTCTGCTGAGCTGCACAG
TAACATGGAGATGGCAGTGGATGGGAGACTGGTCCTTGCCCCGTACGTTGGTGAAAACATGGAAGTCAGCATCTAC
GGCGCTATCATGTATGAAGTCAGGTTTACCCATCTTGCCACATCCTCACATACACCGCCXCAAACAACGAGTT

11735-1-2

AGATCAACCTCTGCTGGTCAGGAGGAATGCCTTCCTTGTCTTGATCTTTGCTTTGACGTTCTCGATAGTRWCAaC
TKKRYTSRAMSKMAAGKGYRATGRWMTTKSYWGWASYKTMWWMRSGRRARAYTTaGaCAYCCCMCCTCWgAGaCGS
AGKACCARGTGCAgAgGTGGACTCTTTCTGGATGTTGTAGTCAGACAGGGTGCGTCCATCTTCCAGCTGTTTCCCA
GCAAAGATCAACCTCTGCTGATCAGGAGGGATGCCTTCCTTATCTTGGATCTTTGCCTTGACATTCTCGATGGTGT
CACTGGGCTCCACCTCGAGGGTGATGGTCTTACCAGTCAGGGTCTTCACGAAGATYTGATCCCACCTCTGAGACG
GAGCACCAGGTGCAGGGTRGACTCTTTCTGGATGTTGTAGTCAGACAGGGTGCGYCCATCTTCCAGCTGcTTTCCS
aGCAAAGATCAACCTCTGCTGGTCAGGAGGRATGCCTTCCTTGTCTTGATCTTTGCTTTGACRTTCTCRATGGTG
TCACTCGGCTCCACTTCGAGAGTGATGGTCTTACCAGTCAGGGTCTTCACGAAGATCTGCATCCCACCTCTAA

11740.2.contig

AAGTCACAAACAGACAAAGATTATTACCAGCTGCAAGCTATATTAGAAGCTGAACGAAGAGACAGAGGTCATGATT
CTGAGATGATTGGAGACCTTCAAGCTCGAATTACATCTTTACAAGAGGAGGTGAAGCATCTCAAACATAATCTCGA
AAAAGTGGAAGGAGAAAGAAAAGAGGCTCAAGACATGCTTAATCACTCAGAAAAGGAAAAAGAATAATTTAGAGATA
GATTTAAACTACAACTTAAATCATTACAACAACGGTTAGAACAAGAGGTAAATGAACACAAAGTAACCAAAGCTC
GTTTAACTGACAAACATCAATCTATTGAAGAGGCAAAGTCTGTGGCAATGTGTGAGATGGAAAAAAGCTGAAAGA
AGAAAGAGAAGCTCGAGAGAAGGCTGAAAATCGGGTTGTTGAGATTGAGAAACAGTGTTCCATGCTAGACGTTGAT
CTGAAGCAATCTCAGCAGAACTAGAACATTTGACTGGAAATAAAGAAAGGATGGAGGATGAAGTTAAGAATCTA

Fig. 15D

11765.2&64.2.contig

CGCCTCCACCATGTCCATCAGGGTGACCCAGAAGTCCTACAAGGTGTCCACCTCTGGCCCCCGGGCCTTCAGCAGC
CGCTCCTACACGAGTGGGCCCCGTTCCCGCATCAGCTCCTCGAGCTTCTCCCGAGTGGGCAGCAGCAACTTTGCGG
GTGGCCTGGGCGGCGGCTATGGTGGGGCCAGCGGCATGGGAGGCATCACCGCAGTTACGGTCAACCAGAGCCTGCT
GAGCCCCCTTGTCTTGAGGTGGACCCCAACATCCAGGCCGTGCGCACCCAGGAGAAGGAGCAGATCAAGACCCCTC
AACAACAAGTTTGCCTCCTTCATAGACAAGGTACGGTTCTTGAGCAGCAGAACAAAGATGCTGGAGACCAAGTGA
GCCTCCTGCAGCAGCAGAAGACGGCTCGAAGCAACATGGACAACATGTTGAGAGCTACATCAACARCTTAGGCG
GCAGCTGGAGACTCTGGGCCAGGAGAAGCTGAAGCTGGAGGCGGAGCTTGGCAACATGCAGGGGCTGGTGGAGGAC
TTCAAGAACAAAGTATGAGGATGAGATCAATAAGCGTACAGAGATGGAGAACGAATTTGTCTCATCAAGAAGGATG
TGGATGAAGCTTACATGAACAAGGTAGAGCTGGAGTCTCGCCTGGAAGGGCTGACCGACGAGATCAACTTCCTCAG
GCAGCTGTATGAAGAGGAGATCCGGGAGCTGCAGTCCCAGATCTCGGACACATCTGTGGTGTGTCCATGGACAAC
AGCCGCTCCCTGGACATGGACAGCATCATTGCTGAGGTCAAGGCACAGTACGAGGATATTGCCAACCGCAGCCGGG
CTGAGGCTGAGAGCATGTACCAGGTCAAGTATGAGGAGCTGCAGAGCCTGGCTGGGAAGCACGGGGATGACCTGCG
GCGCACAAAGACTGAGATCTCTGAGATGAACCCGGAACATCAGCCCGGCTXCAGGCTGAGATTGAGGGCCTCAAAG
GCCAGAXGGCTTXCCTGGAXGXCCGCCAT

11767.2.contig

CCCGGAGCCAGCCAACGAGCGGAAAATGGCAGACAATTTTTCGCTCCATGATGCGTTATCTGGGTCTGGAAACCCA
AACCTCAAGGATGGCCTGGCGCATGGGGGAACAGCCTGCTGGGGCAGGGGGCTACCCAGGGGCTTCCTATCCTG
GGGCTACCCCGGGCAGGCACCCCCAGGGGCTTATCCTGGACAGGCACCTCCAGGCGCCTACCTGGAGCACCTGG
AGCTTATCCCGGAGCACCTGCACCTGGAGTCTACCCAGGGCCACCCAGCGGCCCTGGGGCCTACCCATCTTCTGGA
CAGCCAAGTGCCACCGGAGCCTACCTGCCACTGGCCCCATGGCGCCCCCTGCTGGGCCACTGATTGTGCCTTATA
ACCTGCCTTTGCCTGGGGGAGTGGTGCCTCGCATGCTGATAACAATTCTGGGCACGGTGAAGCCCAATGCAACAG
AATTGCTTTAGATTTCAAAGAGGGAATGATGTTGCCTTCCACTTTAACCACGCTTCAATGAGAACAACAGGAGA
GTCATTGGTTGCAATACAAAGCTGGATAA

11768-1&2

GGGAATGCAACAACTTTATTGAAAGGAAAGTGCAATGAAATTTGTTGAAACCTTAAAGGGGAACTTAGACACCC
CCCCTCRAgCGMAGKACCARGTGCAAgGTGGACTCTTTCTGGATGTTGTAGTCAGACAGGGTRCGWCCATCTTCC
AGCTGTTTTYCCRGCAAAGATCAACCTCTGCTGATCAGGAGGRATGCCTTCCTTATCTTGGATCTTTGCCTTGACAT
TCTCGATGGTGTCACTGGGCTCCACCTCGAGGGTGATGGTCTTACCAGTCAGGGTCTTCACGAAGATYTGATCCC
ACCTCTGAGACGGAGCACCAGGTGCAGGGTRGACTCTTTCTGGATGTTGTAGTCAGACAGGGTGCGYCCATCTTCC
AGCTGcTTTCCSaGCAAAGATCAACCTCTGCTGGTCAGGAGGRATGCCTTCCTTGTCTYTGATCTTTGCTTTGACR
TTCTCAATGGTGTCACTCGGCTCCACTTCGAGAGTGATGGTCTTACCAGTCAGGGTCTTCACGAAGATCTGCATCC
CACCTCTAAGACGGAGCACCAGGTGCAGGGTGGACTCTTTCTGGATGgTTGTAGTCAGACAGGGTGCGTCCATCTT
CCAGCTGTTTCCCAGCAAAGATCAACCT

Fig. 15E

11768-1&2-11735-1&2

AGGTTGATCTTTGCTGGGAAACAGCTGGAAGATGGACGCACCCTGTCTGACTACAACcCATCCAGAAAGAGTCCACC
CTGCACCTGGTGCTCCGTCTTAGAGGTGGGATGCAGATCTTCGTGAAGACCCTGACTGGTAAGACCATCACTCTCG
AAGTGGAGCCGAGTGACACCAATTGAGAAYGTCAARGCAAAGATCCARGACAAGGAAGGCATYCCTCCTGACCAGCA
GAGGTTGATCTTTGCTSGGAAAgCAGCTGGAAGATGGRCGCACCCTGTCTGACTACAACATCCAGAAAGAGTCYAC
CCTGCACCTGGTGCTCCGTCTCAGAGGTGGGATGCAATCTTCGTGAAGACCCTGACTGGTAAGACCATCACCTC
GAGGTGGAGCCAGTGACACCATCGAGAATGTCAAGGCAAAGATCCAAGATAAGGAAGGCATCCCTCCTGATCAGC
AGAGGTTGATCTTTGCTGGGAAACAGCTGGAAGATGGACGCACCCTGTCTGACTACAACATCCAGAAAGAGTCCAC
cTYTGACACYTGGTMCTBCGtCTYaGAGGKGGGRTGcaaaTCTWMGTKWagaCaCtCaCTKKYAAGRYYaTCAMCMW
tgAKKTCgAKYSCASTKWCaCTWTCRAKAAMGTYRWWGCAWagaTCCMAGACAAGGAAGGCATTCTCCTGACCAG
CAGAGGTTGATCT

11769.1.contig

ATGGAGTCTCACTCTGTGACCAAGGCTGGAGCGCTGTGGTGCGATATCGGCTCACTGCAGTCTCCACTTCTGGGT
TCAAGCGATCCTCTGCCTCAGCCTCCCGAGTAGCTGGGACTACAGGCAGGCGTCACCATAATTTTTGTATTTTA
GTAGAGACATGGTTTCGCCATGTTGGCTGGGCTGGTCTCGAACTCCTGACCTCAAGTGATCTGTCTGGCCTCCCA
AAGTGTGGGATTACAGGCGAAAGCCAACGCTCCCGGCCAGGGAACAACCTTTAGAATGAAGGAAATATGCAAAAGA
ACATCACATCAAGGATCAATTAATTACCATCTATTAATTACTATATGTGGGTAATTATGACTATTTCCCAAGCATT
CTACGTTGACTGCTTGAGAAGATGTTTGTCTGCATGGTGGAGAGTGGAGAAGGGCCAGGATTCTTAGGTT

11769.2.contig

AGCGCGGTCTTCCGGCGCGAGAAAGCTGAAGGTGATGTGGCCGCCCTCAACCGACGCATCCAGCTCGTTGAGGAGG
AGTTGGACAGGGCTCAGGAACGACTGGCCACGGCCCTGCAGAAGCTGGAGGAGGCAGAAAAAGCTGCAGATGAGAG
TGAGAGAGGAATGAAGGTGATAGAAAACCGGGCCATGAAGGATGAGGAGAAGATGGAGATTGAGGAGATGCAGCTC
AAAGAGGCCAAGCACATTGCGGAAGAGGCTGACCGCAAATACGAGGAGGTAGCTCGTAAGCTGGTCATCCTGGAGG
GTGAGCTGGAGAGGGCAGAGGAGCGTGCGGAGGTGTCTGAACTAAAATGTGGTGACCTGGAAGAAGAACTCAAGAA
TGTTACTAACAATCTGAAATCTCTGGAGGCTGCATCTGAAAAGTATTCTGAAAAGGAGGACAAATATGAAGAAGAA
ATTAAACTTCTGTCTGACAAACTGAAAGAGGCTGAGACCCGTGCTGAATTTGCAGAGAGAACGGTTGCAAACTGG
AAAAGACAATTGATGACCTGGAAGAGAAACTTGCCACG

11770.1.contig

GTGCACAGGTCCCATTATTGTAGAAAATAATAAATTACAGTGATGAATAGCTCTTCTTAAATTACAAAACAGA
AACCACAAAGAAGGAAGAGGAAAAACCCAGGACTTCCAAGGGTGAAGCTGTCCCCTCCTCCCTGCCACCCTCCCA
GGCTCATTAGTGTCTTGGAAGGGGCAGAGGACTCAGAGGGGATCAGTCTCAGGGGCCCTGGGCTGAAGCGGGTG
AGGCAGAGAGTCTGAGGCCACAGAGCTGGGCAACCTGAGCCGCCTCTCTGGCCCCCTCCCCACCACTGCCCAAA
CCTGTTTACAGCACCTTCGCCCCCTCCCTCTAAACCCGTCCATCCACTCTGCACTTCCAGGCAGGTGGGTGGGCC
AGGCCTCAGCCATACTCCTGGGCGCGGGTTTCGGTGAGCAAGGCACAGTCCAGAGGTGATATCAAGGCCT

Fig. 15F

11770.2.contig

GCAAGGAACTGGTCTGCTCACACTTGCTGGCTTGCGCATCAGGACTGGCTTTATCTCCTGACTCACGGTGCAAAGG
TGCACTCTGCGAACGTTAAGTCCGTCCCCAGCGCTTGGAATCCTACGGCCCCACAGCCGGATCCCCTCAGCCTTC
CAGGTCCTCAACTCCCGTGGACGCTGAACAATGGCCTCCATGGGGCTACAGGTAATGGGCATCGCGCTGGCCGTCC
TGGGCTGGCTGGCCGTATGCTGTGCTGCGCGCTGCCCATGTGGCGCGTGACGGCCTTCATCGGCAGCAACATTGT
CACCTCGCAGACCATCTGGGAGGGCCTATGGATGAACTGCGTGGTGCAGAGCACCAGCCAGATGCAGTGAAGGTG
TACGACTCGCTGCTGGCACTGCCGCAGGACCTGCAGGCGGCCCGCGCCCTCGTCATCATCA

11773.1.contig

TGCAAAAGGGACACAGGGGTTCAAAAATAAAAATTTCTCTTCCCCCTCCCCAACCTGTACCCCAGCTCCCCGACC
ACAACCCCTTCTCTCCCCGGGAAAGCAAGAAGGAGCAGGTGTGGCATCTGCAGCTGGGAAGAGAGAGGCCGGGG
AGGTGCCGAGCTCGGTGCTGGTCTCTTTCAAATATAAATACXTGTGTGAGAACTGGAAAATCCTCCAGCACCCAC
CACCAAGCACTCTCCGTTTTCTGCCGTTGTTGGAGAGGGGCGGGGGGAGGGGCGCCAGGCACCGGCTGGCTGC
GGTCTACTGCATCCGCTGGGTGTGACCCCGCAGCCTCCTGCTGCTCATTGTAGAAGAGATGACACTGGGGGTCC
CCCCGGATGGTGGGGGCTCCCTGGATCAGCTTCCCGGTGTTGGGGTTACACACCAGCACTCCCCACGCTGCCCGT
TCAGAGACATCTTGCACTGTTTGAGGTTGTACAGGCCATGCTTGTCACAGTTG

11778.1.contig

GGGTTGGAGGGACTGGTTCTTTATTTCAAAAAGACACTTGTCAATATTCAGTATCAAAACAGTTGCACTATTGATT
TCTCTTTCTCCCAATCGGCCCCAAAGAGACCACATAAAAGGAGAGTACATTTTAAGCCAATAAGCTGCAGGATGTA
CACCTAACAGACCTCCTAGAAACCTTACCAGAAAAATGGGGACTGGGTAGGGAAGGAACTTAAAAGATCAACAAAC
TGCCAGCCCACGACTGCAGAGGCTGTACAGCCAGATGGGGTGGCCAGGGTGCCACAAACCCAAAGCAAAGTTTC
AAAATAATATAAAATTTAAAAAGTTTTGTACATAAGCTATTCAAGATTTCTCCAGCACTGACTGATACAAAGCACA
ATTGAGATGGCACTTCTAGAGACAGCAGCTTCAAACCCAGAAAAGGGTGATGAGATGAGTTTCACATGGCTAAATC
AGTGGCAAAAACACAGTCTTCTTTCTTTCTTTCAAGGAGGCAGGAAAGCAATTAAGTGGTCACCTCAACATA
AGGGGGACATGATCCATTCTGTAAGCAGTTGTGAAGGGG

11778-2&30-2

CAGGAACCGGAGCGCGAGCAGTAGCTGGGTGGGCACCATGGCTGGGATCACCACCATCGAGGCGGTGAAGCGCAAG
ATCCAGGTTCTGCAGCAGCAGGCAGATGATGCAGAGGAGCGAGCTGAGCGCCTCCAGCGAGAAGTTGAGGGAGAAA
GGCGGGCCCGGAACAGGCTGAGGCTGAGGTGGCCTCCTGAACCGTAGGATCCAGCTGGTTGAAGAAGAGCTGGA
CCGTGCTCAGGAGCGCTGGCCACTGCCCTGCAAAAGCTGGAAGAAGCTGAAAAAGCTGCTGATGAGAGTGAGAGA
GGTATGAAGGTTATTGAAAACCGGGCCTTAAAAGATGAAGAAAAGATGGAATCCAGGAAATCCAACCTCAAAGAAG
CTAAGCACATTGCAGAAGAGGCAGATAGGAAGTATGAAGAGGTGGCTCGTAAGTTGGTGATCATTGAAGGAGACTT
GGAACGCACAGAGGAACGAGCTGAGCTGGCAGAGTCCCGTTGCCGAGAGATGGATGAGCAGATTAGACTGATGGAC
CAGAACCTGAAGTGTCTGAGTGC

11782.1.contig

ATCTACGTCATCAATCAGGCTGGAGACACCATGTTCAATCGAGCTAAGCTGCTCAATATTGGCTTTCAAGAGGCCT
TGAAGGACTATGATTACAACCTGCTTTGTGTTTCAGTGATGTGGACCTCATTCCGATGGACGACCGTAATGCCTACAG
GTGTTTTTCGCAGCCACGGCACATTTCTGTTGCAATGGACAAGTTCGGGTTTAGCCTGCCATATGTTTCAGTATTTT
GGAGGTGTCTCTGCTCTCAGTAAACAACAGTTTCTTGCCATCAATGGATTCCCTAATAATTATTGGGGTTGGGGAG
GAGAAGATGACGACATTTTTTAACAGATTAGTTTATAAAGGCATGTCTATATCACGTCCAAATGCTGTAGTAGGGAG
GTGTGCAATGATCCGGCATTCAAGAGACAAGAAAAATGAGCCCAATCCTCAGAGGTTTGACCGGATCGCACATACA
AAGGAAACGATGCGCTTCGATGGTTTGAACCTACTTACCTACAAGGTGTTGGATGTCAGAGATACCCGTTATATAC
CCAAATCAC

11782.2.contig

CTAGACCTCTAATTAAGGCACAATCATGCTGGAGAATGAACAGTCTGACCCCGAGGGCCACAGCGAATTTTAGG
GAAGGAGGCAAAGAGGTGAGAAGGGAAAGGAAGGAAGGAAGGAGAACAATAAGAAGTGGAGACGTTGGGTGG
GTCAGGGAGTGTGGTGGAGGCTCGGAGAGATGGTAAACAAACCTGACTGCTATGAGTTTTCAACCCCATAGTCTAG
GGCCATGAGGGCGTCAGTTCTTGGTGGCTGAGGGTCCTTCCACCCAGCCACCTGGGGGAGTGGAGTGGGGAGTTC
TGCCAGGTAAGCAGATGTTGTCTCCCAAGTTCCTGACCCAGATGTCTGGCAGGATAACGCTGACCTGTTCCCTCAA
CAAGGGACCTGAAAGTAATTTTGCTCTTTAC

11783-1 & 2

CCGAATTCAGCGTCAACGATCCYTCCCTTACCATCAAATCAATTGGCCACCAATGGTACTGAACCTACGAGTACA
CCGACTACGGCGGACTAATCTTCAACTCCTACATACTTCCCCATTATTCCTAGAACCAGGCGACCTGCGACTCC
TTGACGTTGACAATCGAGTAGTACTCCCGATTGAAGCCCCATTCTGTATAATAATTACATCACAAGACGTCTTGCA
CTCATGAGCTGTCCCCACATTAGGCTTAAAAACAGATGCAATTCCTGGACGTCTAAGCCAAACCACTTTACCGCT
ACACGACCGGGGTATACTACGGTCAATGCTCTGAAATCTGTGGAGCAAACCACAGTTTCATGCCCATCGTCCCTAG
AATTAATTCCTTAAAAATCTTTGAAATAGGGCCCGTATTTACCCTATAGACCCCTCTACCCCTCTAG

11786.1.contig

GCTCTTCACACTTTTTATTGTTAATTCTCTTCACATGGCAGATACAGAGCTGTCGTCTTGAAGACCACCACTGACCA
GGAAATGCCACTTTTACAAAATCATCCCCCTTTTCATGATTGGAACAGTTTTCTGACCGTCTGGGAGCGTTGAA
GGGTGACCAGCACATTTGCACATGCAAAAAGGAGTGACCCCAAGGCCTCAACCACACTTCCAGAGCTCACCATG
GGCTGCAGGTGACTTGCCAGGTTTGGGGTTCGTGAGCTTTCTTGCTGCTGCGGTGGGGAGGCCCTCAAGAACTGA
GAGGCCGGGGTATGCTTCATGAGTGTTAACATTTACGGGACAAAAGCGCATCATTAGGATAAGGAACAGCCACAGC
ACTTCATGCTTGTGAGGGTTAGCTGTAGGAGCGGGTGAAGGATTCCAGTTTATGAAAATTTAAAGCAAACAACGG
TTTTTAGCTGGGTGGGAAACAGGAAAACGTGATGTCGGCCAATGACCACCATTTTTCTGCCCATGTGAAGGTCCC
CATGAAACC

Fig. 15H

11786.2.contig

CAAGCGCTTGGCGTTTGGACCCAGTTCAGTGAGGTTCTTGGGTTTTGTGCCTTTGGGGATTTTGGTTTGACCCAGG
GGTCAGCCTTAGGAAGGTCTTCAGGAGGAGGCCGAGTTCCCCTTCAGTACCACCCCTCTCTCCCACTTTCCCTCT
CCCGGCAACATCTCTGGGAATCAACAGCATATTGACACGTTGGAGCCGAGCCTGAACATGCCCTCGGCCCCAGCA
CATGGAAAACCCCTTCTTGCCTAAGGTGTCTGAGTTTCTGGCTCTTGAGGCATTTCCAGACTTGAAATTCTCAT
CAGTCCATTGCTCTTGAGTCTTTGCAGAGAACCTCAGATCAGGTGCACCTGGGAGAAAGACTTTGTCCCACTTAC
AGATCTATCTCCTCCCTTGGGAAGGGCAGGGAATGGGGACGGTGTATGGAGGGGAAGGGATCTCCTGCGCCCTTCA
TTGCCACACTTGGTGGGACCATGAACATCTTTAGTGTCTGAGCTTCTCAAATTACTGCAATAGGA

13691.1&2

AGCGTCAAATCAGAATGGAAAAGACTCAAAACCATCATCAACACCAAGATCAAAGGACAAGRATCCTTCAAGAAA
CAGGAAAAAACTCCTAAAACACCAAAAGGACCTAGTTCTGTAGAAGACATTAAAGCAAAAATGCAAGCAAGTATAG
AAAAAGGTGGTTCTCTTCCCAAAGTGAAGCCAAATTCATCAATTATGTGAAGAATTGCTTCCGGATGACTGACCA
AGAGGCTATTCAAGATCTCTGGCAGTGGAGGAAGTCTCTTTAAGAAAATAGTTTAAACAATTTGTTAAAAAATTTT
CCGTCTTATTTTCAATTTCTGTAACAGTTGATATCTGGCTGTCTTTTTATAATGCAGAGTGAGAACTTTCCCTACCG
TGTTTGATAAATGTTGTCCAGGTTCTATTGCCAAGAATGTGTTGTCCAAAATGCCTGTTTAGTTTTTAAAGATGGA
ACTCCACCCCTTGCTTGGTTTTAAGTATGTATGGAATGTTATGATAGGACATAGTAGTAGCGGTGGTCAGACATGG
AAATGGTGGGSMGACAAAAATATACATGTGAAATAA

13692.1&2

TCCGAATTCCAAGCGAATTATGGACAAACGATTCCCTTTTAGAGGATTACTTTTTTCAATTTTCGGTTTTAGTAATCT
AGGCTTTGCCTGTAAAGAATACAACGATGGATTTTAAATACTGTTTGTGGAATGTGTTTAAAGGATTGATTCTAGA
ACCTTTGTATATTTGATAGTATTTCTAATCTTCAATTTCTTTACTGTTTGCAGTTAATGTTTCATGTTCTGCTATGCA
ATCGTTTATATGCACGTTTCTTTAATTTTTTTAGATTTTCTTGGATGTATAGTTTAAACAACAAAAAGTCTATTTA
AAACTGTAGCAGTAGTTTACAGTTCTAGCAAAGAGGAAAGTTGTGGGGTTAACTTTGTATTTTCTTTCTTATAGA
GGCTTCTAAAAAGGTATTTTATATGTTCTTTTAAACAATATTGTGTACAACCTTTAAACATCAATGTTTGGAT
CAAAACAAGACCCAGCTTATTTTCTGC

13693.2

TGTGGTGGCGCGGGCTGAGGTGGAGGCCAGGACTCTGACCCTGCCCCTGCCTTCAGCAAGGCCCCCGGCAGCGCC
GGCCACTACGAAGTCCCGTGGGTGAAAAATATAGGCCAGTAAAGCTGAATGAAATTGTCGGGAATGAAGACACCG
TGAGCAGGCTAGAGGTCTTTGCAAGGGAAGGAAATGTGCCAACATCATCATTGCGGGCCCTCCAGGAACCGGCAA
GACCACAAGCATTCTGTGCTTGGCCCGGGCCCTGCTGGGCCCAGCACTCAAAGATGCCATGTTGGAAGTCAATGCT
TCAAATGACAGGGGCATTGACGTTGTGAGGAATAAAATTTAAATGTTTGCTCAACAAAAAGTCACTCTTCCCAAAG
GCCGACATAAGATCATCATTCTGGATGAAGCAGACAGCATGACCGACGGAGCCCAGCAAGCCTTGAGGAGAACCAT
GGAAATCTACTCTAAACCACTCGTTCGCCCTTGCTTGTAAATGCTTCGGATAAGATCATCGAGCC

13696.1-13744.1

CTTTGCAAAGCTTTTATTTTCATGTCTGCGGCATGGAATCCACCTGCACATGGCATCTTAGCTGTGAAGGAGAAAGC
AGTGCACGAGAAGGAATGAGTGGGCGGAACCAACGGCCTCCACAAGCTGCCTTCCAGCAGCCTGCCAAGGCCATGG
CAGAGAGAGACTGCAAACAAACACAAGCAAACAGAGTCTCTTACAGCTGGAGTCTGAAAGCTCATAGTGGCATGT
GTGAATCTGACAAAATTAAGTGTGCATAGTCCATTACATGCATAAAACACTAATAATAATCCTGTTTACACGTG
ACTGCAGCAGGCAGGTCCAGCTCCACCACTGCCCTCCTGCCACATCACATCAAGTGCCATGGTTTAGAGGGTTTTT
CATATGTAATTCTTTTATTCTGTAAAAGGTAACAAAATATACAGAACAAAACCTTCCCTTTTTAAACTAATGTTA
CAAATCTGTATTATCACTTGGATATAAATAGTATATAAGCTGATC

13700.1

CAAGGGATATATGTTGAGGGTACRGRGTGACACTGAACAGATCACAAAGCACGAGAAACATTAGTTCTCTCCCTCC
CCAGCGTCTCCTTCGTCTCCCTGGTTTTCCGATGTCCACAGAGTGAGATTGTCCCTAAGTAACTGCATGATCAGAG
TGCTGKCTTTATAAGACTCTTCATTACAGCGTATCCAATTCAGCAATTGCTTCATCAAATGCCGTTTTTGCCAGGCT
ACAGGCCTTTTCAGGAGAGTTTGAATCTCATAGTAAAAGACTGAGAAATTTAGTGCCAGACCAAGACGAATTGGG
TGTGTAGGCTGCATTNCTTTCTTACTAATTTCAAATGCTTCCTGGTAAGCCTGCTGGGAGTTCGACACAAGTGTT
TGTTTGTTGCTCCAGATGCCACTTCAGAAAGATACCTAAAATAATCTCCTTTCATTTTCAAAGTAGAACAC

13700.2

TCCGGAGCCGGGGTAGTCGCCGCCGCCGCCGGTGCAGCCACTGCAGGCACCGCTGCCGCCGCCTGAGTAGTGG
GCTTAGGAAGGAAGAGGTCATCTCGCTCGGAGCTTCGCTCGGAAGGGTCTTTGTTCCCTGCAGCCCTCCACGGGA
ATGACAATGGATAAAAGTGAGCTGGTACAGAAAGCCAACTCGCTGAGCAGGCTGAGCGATATGATGATATGGCTG
CAGCCATGAAGGCAGTCACAGAACAGGGGCATGAACTCTCCAACGAAGAGAGAAATCTGCTCTCTGTTGCCTACAA
GAATGTGGTAAGGCCGCCGCCGCTCTTCTGGCGTGTCTCTCCAGCATTGAGCAGAAAACAGAGAGGAATGAGA
AGAAGCAGCAGATGGGCAAAGAGTACCGTGAGAAGATAGAGGCAGAACTGCAGGACATCTGCAATGATGTTCTGGA
GCTTGTTGGACAAATATCTTATTCCAATGCTACACAACCCAGAAA

13701.1

AAAAAGCAGCARGTTCAACACAAAATAGAAATCTCAAATGTAGGATAGAACAAAACCAAGTGTGTGAGGGGGGAAG
CAACAGCAAAAGGAAGAAATGAGATGTTGCAAAAAAGATGGAGGAGGGTCCCCCTCTCCTCTGGGGACTGACTCAA
ACACTGATGTGGCAGTATACACCATTCAGAGTCAGGGGTGTTCAATCTTTTTTGGGAGTAAGAAAAGGTGGGGAT
TAAGAAGACGTTTCTGGAGGCTTAGGGACCAAGGCTGGTCTCTTTCCCCCTCCCAACCCCTTGATCCCTTTCTC
TGATCAGGGGAAAGGAGCTCGAATGAGGGAGGTAGAGTTGGAAAGGGAAAGGATTCCACTTGACAGAATGGGACAG
ACTCCTTCCCA

13701.2

TGGCAATAGCACAGCCATCCAGGAGCTCTTCARGCGCATCTCGGAGCAGTTCACTGCCATGTTCCGCCGGAAGGCC
TTCCTCCACTGGTACACAGGCGAGGGCATGGACGAGATGGAGTTCACCGAGGCTGAGAGCAACATGAACGACCTCG
TCTCTGAGTATCAAGCAGTACCAGGATGCCACCGCAGAAGAGGAGGAGGATTTCCGGTGAGGAGGCCGAAGAGGAGG
CCTAAGGCAGAGCCCCATCACCTCAGGCTTCTCAGTTCCCTTAGCCGTCTTACTCAACTGCCCCTTTCTCTCTCC
TCAGAATTTGTGTTTGCTGCCTCTATCTGTTTTTTGTTTTTCTTCTGGGGGGTCTAGAACAGTGCCTGGCACA
TAGTAGGCGCTCAATAAATACTTGGTTGNTGAATGTCTCCT

13702.2

AGCTGGCGCTAGGGCTCGGTTGTGAAATACAGCGTRGTCAGCCCTTGCCTCAGTGTAGAAACCCACGCCTGTAAG
GTCGGTCTTCGTCCATCTGCTTTTTTCTGAAATACACTAAGAGCAGCCACAAAACCTGTAACCTCAAGGAAACCATA
AAGCTTGGAGTGCCTTAATTTTAAACCAGTTTCCAATAAAACGGTTTACTACCT

13704.2-13740.2

GGAGATGAAGATGAGGAAGCTGAGTCAGCTACGGGCARGCGGGCAGCTGAAGATGATGAGGATGACGATGTGATA
CCAAGAAGCAGAAGACCGACGAGGATGACTAGACAGCAAAAAGGAAAAGTTAAA

13706.1

GATGAAAATTAATACTTAAATTAATCAAAAGGCACTACGATACCACCTAAAACCTACTGCCTCAGTGGCAGTAKG
CTAAKGAAGATCAAGCTACAGSACATYATCTAATATGAATGTTAGCAATTACATAKCARGAAGCATGTTTGCTTTC
CAGAAGACTATGGNACAATGGTCATTWGGGCCCAAGAGGATATTTGGCCNGGAAAGGATCAAGATAGATNAANGTA
AAG

13706.2

GAGTAGCAACGCAAAGCGCTTGGTATTGAGTCTGTGGGSGACTTCGGTTCCGGTCTCTGCAGCAGCCGTGATCGCT
TAGTGGAGTGCTTAGGGTAGTTGGCCAGGATGCCGAATATCAAAATCTTCAGCAGGCAGCTCCCACCAGGACTTAT
CTCASAAAATTGCTGACCGCCTGGGCCTGGAGCTAGGCAAGGTGGTGAATAAGAAATTCAGCAACCAGGAGACCTG
TGTGGAAATTGGTGAAAGTGTACCGTGGAGAGGATGTCTACATTGTTGAGAGTGGNTGTGGCGAAATCAATGACAA
TTTAATGGAGCTTTTGATCATGATTAATGCCTGCAAGATTGCTTCAGCCAGCCGGGTTACTGCAGTCATCCCATGC
TTCCCTTATGCCCCGGCAGGATAAGAAAGATNAGAGCCGGGCCCAATCTCAGCCAAGCTTGGTGCAAATATGCT
ATCTGTAGCAGTGCAGATCATATTATCACCATGGACCTACATGCTTCTCAAATTCANGGCTTTTT

13707.3

ATGCAAAAGGGGACACAGGGGGTTCAAAAATAAAAATTTCTCTTCCCCCTCCCCAACCTGTACCCCAGCTCCCCG
ACCACAACCCCTTCTCCCCGGGAAAGCAAGAAGGAGCAGGTGTGGCATCTGCAGCTGGGAAGAGAGAGGCCG
GGGAGGTGCCGAGCTCGGTGCTGGTCTCTTTCCAAATATAAATACGTGTGTCAGAACTGGAAAATCCTCCAGCACC
CACCACCCAAGCACTCTCCGTTTTCTGCCGGTGTGGAGAGGGGCGGNGGGCAGGGGCGCCAGGCACCGGCTGGC
TGCGGTCTACTGCATCCGCTGGGTGTGCACCCCGCA

13710.2

AGGTTGGAGAAGGTCATGCAGGTGCAGATTGTCCAGGSKCAGCCACAGGGTCAAGCCCAACAGGCCAGAGTGGCA
CTGGACAGACCATGCAGGTGATGCAGCAGATCATCTAACACAGGAGAGATCCAGCAGATCCCGGTGCAGCTGAA
TGCCGGCCAGCTGCAGTATATCCGCTTAGCCCAGCCTGTATCAGGCACTCAAGTTGTGCAGGGACAGATCCAGACA
CTTGCCACCAATGCTCAACAGATTACACAGACAGAGGTCCAGCAAGGACAGCAGCAGTTCAAGCCAGTTCACAAGA
TGGACAGCAGCTCTACCAGATCCAGCAAGTCACCATGCCTGCGGGCCANGACCTCGCCAGCCCATGTTTCATCCAGT
CAAGCCAACCAGCCCTTCNACGGGCAGGCCCCCCAGGTGACCGGCGACTGAAGGGCCTGAGCTGGCAAGGCCAANG
ACACCCAACACAATTTTTGCCATACAGCCCCCAGGCAATGGGCACAGCCTTTCTTCCCAGAGGAC

13710-1

TGAGATTTATTGCATTTTCATGCAGCTTGAAGTCCATGCAAAGGRGACTAGCACAGTTTTTAATGCATTTAAAAAT
AAAAGGGAGGTGGGCAGCAAAACACACAAAGTCCTAGTTTCTGGGTCCCTGGGAGAAAAGAGTGTGGCAATGAATC
CACCCACTCTCCACAGGGAATAAATCTGTCTCTTAAATGCAAAGAATGTTTCCATGGCCTCTGGATGCAATACAC
AGAGCTCTGGGGTCAGAGCAAGGGATGGGGAGAGGACCACGAGTGAAAAAGCAGCTACACACATTCACCTAATTCC
ATCTGAGGGCAAGAACAACGTGGCAAGTCTTGGGGTAGCAGCTGTT

13711.1

TCCAGACATGCTCCTGTCTAGGCGGGGAGCAGGAACCCAGACCTGCTATGGGAAGCAGAAAGAGTTAAGGGAAGGT
TTCCTTTTCATTCTGTTCTTCTCTTTTGCTTTTGAACAGTTTTTAAATATACTAATAGCTAAGTCATTTGCCAGC
CAGGTCCCGGTGAACAGTAGAGAACAAGGAGCTTGCTAAGAATTAATTTTGCTGTTTTTACCCCATTCAAACAGA
GCTGCCCTGTTCCCTGATGGAGTTCATTCTGCCAGGGCACGGCTGAGTAACACGAAGCCATTCAAGAAAGGCGG
GTGTGAAATCACTGCCACCCCATGGACAGACCCCTCACTCTTCTTCTTAGCCGCAGCGCTACTTAATAAATATAT
TTATACTTTGAAATTATGATAACCGATTTTTCCCATGCGGCATCTAAGGGCACTTGCCAGCTCTTATCCGGACAG
TCAAGCACTGTTGTTGGACAACAGATAAAGGAAAAGAAAAAGAAGAAAACAACCGCAACTTCTGT

13711.2

TGAGACGGACCACTGGCCTGGTCCCCCTCATKTGCTGTCGTAGGACCTGACATGAAACGCAGATCTAGTGGCAGA
GAGGAAGATGATGAGGAACCTTCTGAGACGTCGGCAGCTTCAAGAAGAGCAATTAATGAAGCTTAACCTCAGGCCTGG
GACAGTTGATCTTGAAAGAAGAGATGGAGAAAGAGAGCCGGGAAAGGTCACTCTGTAGCCAGTCGCTACGATTC
TCCCATCAACTCAGCTTCACATATTCATCATCTAAACTGCATCTCTCCCTGGCTATGGAAGAAATGGGCTTCAC
CGGCCTGTTTCTACCGACTTCGCTCAGTATAACAGCTATGGGGATGTCAGCGGGGAGTGCGAGATTACCAGACAC
TTCCAGATGGCCACATGCCTGCAATGAGAATGGACCGAGGAGTGTCTATGCCCAACATGTTGGAACCAAAGATATT
TCCATATGAAATGCTCATGGTGACCAACAGAGGGCCGAAACCAATCTCAGAGAGGTGGACAGAA

13713.1&2

TCACTTTATTTTTCTTGTATAAAAACCTATGTTGTAGCCACAGCTGGAGCCTGAGTCCGCTGCACGGAGACTCTG
GTGTGGGTCTTGACGAGGTGGTCAGTGAACCTCTGATAGGGAGACTTGGTGAATACAGTCTCCTTCCAGAGGTGCG
GGGTGAGGTAGCTGTAGGTCTTAGAAATGGCATCAAAGGTGGCCTTGCGAAGTTGCCAGGGTGGCAGTGCAGCC
CCGGGCTGAGGTGTAGCAGTCATCGATACCAGCCATCATGAG

13715.4

CTGGAATATAGACCCGTGATCGACAAAACCTTTGAACGAGGCTGACTGTGCCACCGTCCCGCCAGCCATTGCTCCT
ACTGATGAGACAAGATGTGGTGATGACAGAATCAGCTTTTGTAAATATGTATAATAGCTCATGCATGTGTCCATGT
CATAACTGTCTTCATACGCTTCTGCACTCTGGGGAAGAAGGAGTACATTGAAGGGAGATTGGCACCTAGTGGCTGG
GAGCTTGCCAGGAACCCAGTGGCCAGGGAGCGTGGCACTTACCTTTGTCCCTTGCTTCATTCTTGTGAGATGATAA
AACTGGGCACAGCTCTTAAATAAAATATAAATGAACA

13717.1&2

TGAATGGGGAGGAGCTGACCCAGGAAATGGAGCTTGNGGAGACCAGGCCTGCAGGGGATGGAACCTTCCAGAAGTG
GGCATCTGTGGTGGTGCCTCTTGGGAAGGAGCAGAAGTACACATGCCATGTGGAACATGAGGGGCTGCCTGAGCCC
CTCACCCCTGAGATGGGGCAAGGAGGAGCCTCCTTCATCCACCAAGACTAACACAGTAATCATTGCTGTTCCGGTTG
TCCTTGGAGCTGTGGTCATCCTTGGAGCTGTGATGGCTTTTGTGATGAAGAGGAGGAGAAACACAGGTGGAAAAGG
AGGGGACTATGCTCTGGCTCCAGGCTCCAGAGCTCTGATATGTCTCTCCAGATTGTAAAGTGTGAAGACAGCTG
CCTGGTGTGGACTTGGTGACAGACAATGTCTTCACACATCTCCTGTGACATCCAGAGACCTCAGTTCTCTTTAGTC
AAGTGTCTGATGTTCCCTGTGAGTCTGCGGGCTCAAAGTGAAGAACTGTGGAGCCCAGTCCACCCCTGCACACCAG
GACCCTATCCCTGCACTGCCCTGTGTTCCCTTCCACAGCCAACCTTGCTGCTCCAGCCAAACATTGGTGGACATCT
GCAGCCTGTCAGCTCCATGCTACCCTGACCTTCAACTCCTCACTTCCCACTGAGAATAATAATTTGAATGTGGGT
GGCTGGAGAGATGGCTCAGCGCTGACTGCTCTTCCAAAGGTCTGAGTTCAAATCCAGCAACCACATGGTGGCTC
ACAACCATCTGTAATGGGATCTAATACCCTCTTCTGCAGTGTCTGAAGACASCTACAGTGTACTTACATATAATAA
TAAATAAG

Fig. 15M

13719.1&2

GGCCGGGCGCGCGCGCCCCGCCACACGCACGCCGGGCGTGCCAGTTTATAAAGGGAGAGAGCAAGCAGCGAGTCT
TGAAGCTCTGTTTGGTGCTTTGGATCCATTTCCATCGGTCCTTACAGCCGCTCGTCAGACTCCAGCAGCCAAGATG
GTGAAGCAGATCGAGAGCAAGACTGCTTTTCAGGAAGCCTTGGACGCTGCAGGTGATAAACTTGTAGTAGTTGACT
TCTCAGCCACGTGGTGTGGGCCTTGCAAAATGATCAAGCCTTTCTTTTATTCCCTCTCTGAAAAGTATTCCAACGT
GATATTCCTTGAAGTAGATGTGGATGACTGTCAGGATGTTGCTTCAGAGTGTGAAGTCAAATGCATGCCAACATTC
CAGTTTTTTAAGAAGGGACAAAAGGTGGGTGAATTTTCTGGAGCCAATAAGGAAAAGCTTGAAGCCACCATTAAATG
AATTAGTCTAATCATGTTTTCTGAAAATATAACCAGCCATTGGCTATTTAAACTTGTAATTTTTTTAATTTACAA
AAATATAAAATATGAAGACATAAACCCMGTGCCATCTGCGTGACAATAAACATTAATGCTAACACTT

13721.1

TCACATAAGAAATTTAAGCAAGTTACRCTATCTTAAAAACACAACGAATGCATTTTAATAGAGAAACCCTTCCCT
CCCTCCACCTCCCTCCCCACCCTCCTCATGAATTAAGAATCTAAGAGAAGAAGTAACCATAAAACCAAGTTTTGT
GGAATCCATCATCCAGAGTGCTTACATGGTGATTAGGTTAATATTGCCTTCTTACAAAATTTCTATTTTTAAAAAA
ATTATAACCTTGATTGCTTATTACAAAAAATTCAGTACAAAAGTTCAATATATTGAAAAATGCTTTTCCCTCCC
TCACAGCACCGTTTTATATATAGCAGAGAATAATGAAGAGATTGCTAGTCTAGATGGGGCAATCTTCAAATTACAC
CAAGACGCACAGTGGTTTTATTACCCTCCCCTTCTCATAAG

13721.2

GGAAAGGATTCAAGAATTAGAGGACTTGCTTGCTRRAGAAAAAGACAACCTCTCGTCGCATGCTGACAGACAAAGAG
AGAGAGATGGCGGAAATAAGGGATCAAATGCAGCAACAGCTGAATGACTATGAACAGCTTCTTGATGTAAAGTTAG
CCCTGGACATGGAAATCAGTGCTTACAGGAACTCTTAGAAGGCGAAGAAGAGAGGTTGAAGCTGTCTCCAAGCCC
TTCTTCCCGTGTGACAGTATCCCGAGCATCCTCAAGTCGTAGTGTACCGTACAACCTAGAGGAAAGCGGAAGAGGGT
TGATGTGGAAGAATCAGAGGCGAAGTAGTAGTGTTAGCATCTCTCATTCCGCCTCAACCACTGGAAATGTTTGCAT
CGAAGAAATTGATGTTGATGGGAAATTTATCCCGCTTGAAGAACACTTCTGAACAGGATCAACCAATGGGAAGGCT
TGGGAGATGATCAGAAAAATTGGAGACACATCAGTCAGTTATAAATATACCTCAA

13723.1

CATGGGTTTCACCAGGTTGGCCAGGCTGCTCTTGAACCTCTGACCTCAGGTGATCCACCCGCCTCGGCCTCCAAA
GTGCTGGGATTACAGGCGTGAGCCACCACGCCCGGCCCCAAAGCTGTTTCTTTGTCTTTAGCGTAAAGCTCTCC
TGCCATGCAGTATCTACATAACTGACGTGACTGCCAGCAAGCTCAGTCACTCCGTGGTCTTTTTCTCTTTCCAGTT
CTTCTCTCTCTTCAAGTTCTGCCTCAGTGAAAGCTGCAGGTCCCAGTTAAGTGATCAGGTGAGGGTTCTTTGA
ACCTGGTTCTATCAGTCGAATTAATCCTTCATGATGG

Fig. 15N

13723.2

GATGTGTTGGACCCTCTGTGTCAAAAAAACCTCACAAAGAATCCCCTGCTCATTACAGAAGAAGATGCATTTAAA
ATATGGGTTATTTTCAACTTTTATCTGAGGACAAGTATCCATTAATTATTGTGTCAGAAGAGATTGAATACCTGC
TTAAGAAGCTTACAGAAGCTATGGGAGGAGTTGGCAGCAAGAACAATTTGAACATTATAAAATCAACTTTGATGA
CAGTAAAAATGGCCTTTCTGCATGGGAACCTATTGAGCTTATTGGAATGGACAGTTTAGCAAAGGCATGGACCGG
CAGACTGTGTCTATGGCAATTAATGAAGTCTTTAATGAACCTATATTAGATGTGTTAAAGCAGGGTTACATGATGA
AAAAGGGCCACAGACGGAAAACTGGACTGAAAGATGGTTTGTACTAAAACCCAACATAATTTCTTACTATGTGAG
TGAGGATCTGAAGGATAAGAAAGGAGACATTCTCTTGATGAAATTGCTGTGTAGAAGTCCTTGCCTGACAAAAG
ATGGAAGAAATGCCTTTT

13725.1

GA CTGGTTCTTTATTTCAAAAAGACACTTGTCAATATTCAGTRTCAAAACAGTTGCACTATTGATTTCTCTTTCTC
CCAATCGGCCCCAAAGAGACCACATAAAAGGAGAGTACATTTTAAGCCAATAAGCTGCAGGATGTACACCTAACAG
ACCTCCTAGAAACCTTACCAGAAAATGGGACTGGGTAGGGAAGGAACTTAAAAGATCAACAACTGCCAGCCCA
CGGACTGCAGAGGCTGTACAGCCAGATGGGGTGGCCAGGGTGCCACAAACCCAAAGCAAAGTTTCAAATAATAT
AAAATTTAAAAAGTTTTGTACATAAGCTATTCAAGATTTCTCCAGCACTGACTGATACAAAGCACAATTGAGATGG
CACTTCTAGAGACAGCAGCTTCAAACCCAGAAAAGGGTGATGAGATGAAGTTTACATGGCTAAATCAGTGCCAAA
AACACAGTCTTCTTTCTTTCTTTCTTTCAAGGANGCAGGAAAGCAATTAAGTGGTCACCTTAACATAAGGGGGAC

13725.2

TGGGTGGGCACCATGGCTGGGATCACCACCATCGAGGCGGTGAAGCGCAAGATCCAGGTTCTGCAGCAGCAGGCAG
ATGATGCAGAGGAGCGAGCTGAGCGCCTCCAGCGAGAAGTTGAGGGAGAAAGGCGGGCCCGGGAACAGGCTGAGGC
TGAGGTGGCCTCCTTGAACCGTAGGATCCAGCTGGTTGAAGAAGAGCTGGACCGTGCTCAGGAGCGCCTGGCCACT
GCCCTGCAAAAGCTGGAAGAAGCTGAAAAAGCTGCTGATGAGAGTGAGAGAGGTATGAAGGTTATTGAAAACCGGG
CCTTAAAAGATGAAGAAAAGATGGAACCTCAGGAAATCCAACCTCAAAGAAGCTAAGCACATTGCAGAAGAGGCAGA
TAGGAAGTATGAAGAGGTGGCTCGTAAGTTGGTGATCATTGAAGGAGACTTGGAACCGCACAGAAGGAACGAGCTT
GAGCTTGGCAAAAGTCCCGTTGCCAGAGATGGGATGAACCAGATTAGACTGATGGACCANAACC

13726.1&2

AGGGGCNGCGGGTGCGTGGGCCACTGGGTGACCGACTTAGCCTGGCCAGACTCTCAGCACCTGGAAGCGCCCCGAG
AGTGACAGCGTGAGGCTGGGAGGGAGGACTTGGCTTGAGCTTGTTAACTCTGCTCTGAGCCTCCTTGTCGCTGC
ATTTAGATGGCTCCCGCAAAGAAGGGTGGCGAGAAGAAAAAGGGCCGTTCTGCCATCAACGAAGTGGTAACCCGAG
AATACACCATCAACATTCACAAGCGCATCCATGGAGTGGGCTTCAAGAAGCGTGACCTCGGGCACTCAAAGAGAT
TCGGAATTTGCCATGAAGGAGATGGGAACCTCAGATGTGCGCATTGACACCAGGCTCAACAAAGCTGTCTGGGCC
AAAGGAATAAGGAATGTGCCATACCGAATCCGGTGTGCGGCTGTCCAGAAAACGTAATGAGGATGAAGATTACCA
AATAAGCTATATACTTTGGTTACCTATGTACCTGTTACCACTTTCAAAAATCTACAGACAGTCAATGTGGATGAGA
ACTAATCGCTGATCGTCAGATCAAATAAAGTTATAAAAT

Fig. 150

13727.1

TCGGGAGCCACACTTGGCCCTCTTCCTCTCCAAAGSGCCAGAACCTCCTTCTCTTTGGAGAATGGGGAGGCCTCTT
GGAGACACAGAGGGTTTACCTTGGATGACCTCTAGAGAAATTGCCCAAGAAGCCCACCTTCTGGTCCCAACCTGC
AGACCCACAGCAGTCAGTTGGTCAGGCCCTGCTGTAGAAGGTCACTTGGCTCCATTGCCTGCTTCCAACCAATGG
GCAGGAGAGAAGGCCTTTATTTCTCGCCACCCATTCTCTGTACCAGCACCTCCGTTTTTCAGTCAGTGTTGTCC
AGCAACGGTACCGTTTACACAGTCACCTCAGACACACCATTTACCTCCCTTGCCAAGCTGTTAGCCTTAGAGTGA
TTGCAGTGAACACTGTTTACACACCGTGAATCCATTCCCATCAGTCCATTCCAGTTGGCACCAGCCTGAACCATTT
GGTACCTGGTGTTAACTGGAGTCCTGTTTACAAGGTGGAGTCGGGGCTTGCTGACTTCTCTTCATTTGAGGGCAC

13727.2

ACCTAGACAGAAGGTGGGTGAGGGAGGACTGGTAGGAGGCTGAGGCAATTCCTTGGTAGTTTGTCTGAAACCCTA
CTGGAGAAGTCAGCATGAGGCACCTACTGAGAGAAGTGCCAGAAACTGCTGACTGCATCTGTTAAGAGTTAACAG
TAAAGAGGTAGAAGTGTTTCTGAATCAGAGTGGAAGCGTCTCAAGGGTCCCACAGTGGAGGTCCCTGAGCTACC
TCCCTTCCGTGAGTGGGAAGAGTGAAGCCCATGAAGAACTGAGATGAAGCAAGGATGGGGTTCCTGGGCTCCAGGC
AAGGGCTGTGCTCTCTGCAGCAGGGAGCCCCACGAGTCAGAAGAAAAGAACTAATCATTTGTTGCAAGAAACCTTG
CCCGGATACTAGCGGAAAACTGGAGGCGNGGTGGGGGCACAGGAAAGTGGAAGTGATTTGATGGAGAGCAGAGAA
GCCTATGCACAGTGGCCGAGTCCACTTGTAAGTG

13728.1&2

TTCAAGCAATTGTAACAAGTATATGTAGATTAGAGTGAGCAAAATCATATACAATTTTCATTTCCAGTTGCTATTT
TCCAAATTGTTCTGTAATGTCGTTAAATTACTTAAAAATTAACAAAGCCAAAAATTATATTTATGACAAGAAAGC
CATCCCTACATTAATCTTACTTTTCCACTCACCGGCCATCTCCTTCCTCTTTTTCTTAACCTATGCCATTAAACT
GTTCTACTGGGCCGGGCGTGTGGCTCATGCCTGTAATCCCAGCATTTTGGGAGGCCAAGGCAGGCGGATCATGAGG
TCAAGAGATTGAGACCATCCTGGCCAACATGGTGAAACCCCGCCTCGACTAAGAATACAAAAATTAGCTGGGCATG
GTGGCGCATGCCTGTAGTCTCAGCTACTCGGGAGGCTGAGGCAGAAGAATCGCTTGAACCCGGGAGGCAGAGGATG
CAGTGAGCCCCGATCGCGCCACTGCACTCTAGCCTGGGCGACAGACTGAGACTCTGCTC

13731.1&2

TGTGCCAGTCTACAGGCCTATCAGCAGCGACTCCTTCAGCAACAGATGGGGTCCCCTGTTGAGCCCAACCCCATGA
GCCCCCAGCAGCATATGCTCCCAAATCAGGCCAGTCCCCACACCTACAAGGCCAGCAGATCCCTAATTCTCTCTC
CAATCAAGTGCGCTCTCCCCAGCCTGTCCCTTCTCCACGGCCACAGTCCCAGCCCCCCCCACTCCAGTCTTCCCCA
AGGATGCAGCCTCAGCCTTCTCCACACCACGTTTCCCCACAGACAAGTTCCCCACATCCTGGACTGGTAGTTGCC
AGGCCAACCCCATGGAACAAGGGCATTGTCAGCC

Fig. 15P

13734.1&2

TGTA AAAA ACTTGT TTTTAA TTTTGT ATAAATAA AGGTGGTCCATGCCACGGGGGCTGTAGGAAATCCAAGCAGACCA
GCTGGGGTGGGGGATGTAGCCTACCTCGGGGACTGTCTGTCTCAAAACGGGCTGAGAAGGCCCGTCAGGGGCCAG
GTCCACAGAGAGGCTGGGATACTCCCCAACCCGAGGGGAGACTGGGCAGTGGGGAGCCCCATCGTCCCCAGAG
GTGGCCACAGGCTGAAGGAGGGGCTGAGGCACCGCAGCCTGCAACCCCCAGGGCTGCAGTCCACTA ACTTTTACAGA
ATAAAAGGAACATGGGGATGGGGAAAAAGCACCAGGTGAGGCAGGGCCCGAGGGCCCCAGATCCCAGGAGGGCCAGGA
CTCAGGATGCCAGCACCACCTAGCAGCTCCACAGCTCCTGGCACAGGAGGCCGCCACGGATTGGCACAGGCCGCTGC
TGGCCATCACGCCACATTTGGAGAACTTGTCCGACAGAGGTGAGCTCGGAGGAGCTCCTCGTGGGCACACACTGTACG
AACACAGATCTCCTTGTTAATGACGTACACACGGCGGAGGCTGCGGGGACAGGGCACGGGAGGTCTCAGCCCCACTT

13736.2

ATGGCTGCTGGATTTAGGTGGTAATAGGGGCTGTGGGCCATAAATCTGAAGCCTTGAGAACCTTGGGTCTGGAGAGCCA
TGAAGAGGGAAGGAAAAGAGGGCAAGTCTGAACCTAACCAATGACCTGATGGATTGCTCGACCAAGACACAGAAGTGA
AGTCTGTGTCTGTGCACTTCCACAGACTGGAGTTTTTGGTGTGTAATAGAGCCAGTTGCTAAAAAATTGGGGGTTGG
TGAAGAAATCTGATTGTTGTGTGATTCAATGTGTGATTTTAAAAATAAACAGCAACAACAATAAAACCCCTGACTGGC
TGTTTTTCCCTGTATTCTTTACAATATTTTTTGACCCTCTGAAAATTATTATACTTCACCTAAATGGAAGACTGCTG
TGTTTGTGGAAATTTTGTAAATTTTTAATTTATTTTATTCTCTCTCTTTTATTTTGCCTGCAGAATCCGTTGAGAGA
CTAATAAGGCTTAATATTTAATTGATTTGTTTAATATGTATATAAAT

13744.2-13696.2

GGCATGCGAGCGCACTCGGCGGACGCAAGGGCGGCGGGGAGCACACGGAGCACTGCAGGCGCCGGGTTGGGACAGCGTG
TTCGCTGCTGCTGGATAGTCGTGTTTTCGGGGATCGAGGATACTCACCAGAAACCGAAAATGCCGAAACCAATCAATGT
CCGAGTTACCACCATGGATGCAGAGCTGGAGTTTGCAATCCAGCCAAATACAACCTGGAAAACAGCTTTTTGATCAGGTG
GTAAAGACTATCGGCCTCCGGGAAGTGTGGTACTTTGGCCTCCACTATGTGGATAATAAAGGATTTCTACCTGGCTGA
AGCTGGATAAGAAGGTGTCTGCCAGGAGGTGAGGAAGGAGAATCCCTCCAGTTCAAGTTCCGGGGCCAAAGTTCTACC
CTGAAGATGTGGCTGAGGAGCTCATCCAGGACATCACCAGAACTTTTCTTCTTCAAGTGAAGGAAGGAATCCTTAG
CGATGAGATCTACTGCCCCCTTGARACTGCCGTGCTCTTGGGGTCTACGCTTGTGCATGCCAAGTTTGGGGACTACC
ACCAAGAAG

13746.1&2-13720.1&2

GAAGGAGTCGGGATACTCAGCATTGATGCACCCCAATTTCAAAGCGGCATTCTTCGGCAGGTCTCTGGGACAATCTCTA
GGGTCACTACCTGGAACTCGTTAGGGTACAACCTGAATGCTGAAAGGAAAGAACACCTGCAGAACCGGACAGAAATTCA
CCCCGGCGATCAGCTGATTGATCTCGGTGACACAGAAGTCATGGCTAAAGATGACGAGGACGTTGTCAATTCCTGGGC
TTTTCGAAGTGAGTCCAGCAGCAGTCTGAGGTATTCGGGCCGGTTATGCACCTGGACCACCAGCACCAGCTCCCGGGG
GCCAGGTGCCAGCCTTATCTACATTCTCAGGGTCTGATCAAAGTTCAGCTGGTACACCAGGGACCGGTACCGCAGCG
TCAGGTTGTCCGCTCGGGCTGGGGGACCGCCGGGACCAGGGAAGCCGCCGACACGTTGGAGACCCTGCGGATGCCACA
GCCACAGAGGGGTGGTCCCCACCGCGGGCCGCCGGCACCCCGCGGGTTCGGCGTCCAGCAACGGTGGGGCGAGGGCCT
CGTTCTTCTTTGTGCCCCATTGCTGCTCCAGAGGACGAAGCCGACGGCGGCCACCACGAGCGTCAGGATTAGCACCTT
CCGTTTGTAGATGCCGAACCTCATGGTCTCCAGGGCCGGGAGCGCAGCTACAGCTCGAGCGTCGGCGCCGCCGCTAGGA
GCCGCGGCTCGGCTTCGTCTCCGTCTCTCATTACGACACACGGGTCCCGAAAAAGTCTAGCCSCGGTCCCAACCGC
ACCCTAGCTTCGTTACCTGCGCTCGCTTG

Fig. 15Q

14347.1

CAGATTTTATTTGCAGTCGTCAGTGGGGCCGTTTCTTGCTGCTTATTTGTCTGCTAGCCTGCTCTTCCAGCTGCA
TGGCCAGGCGCAAGGCCTTGATGACATCTCGCAGGGCTGAGAAATGCTTGGCTTGTGGGCCAGAGCAGATTCCGC
TTTGTTCAAAAGGTCTCCAGGTCATAGTCTGGCTGCTCGGTATCTCAGAGAGCTCAAGCCAGTCTGGTCCTTGC
TGTATGATCTCCTTGAGCTCTTCCATAGCCTTCTCCTCCAGCTCCCTGATCTGAGTCATGGCTTCGTTAAAGCTGG
ACATCTGGGAAGACAGTTTCTCCTCTTCTTGGATAAATTGCCTGGAATCAGCGCCCCGTTAGAGCAGGCTTCCAT
CTCTTCTGTTTCCATTTGAATCAACTGCTCTCCACTGGGGCCACTGTGGGGGCTCAGCTCCTTGACCCTGCTGCAT
ATCTTAAGGGTGTTTAAAGGATATTCACAGGAGCTTATGCCTGGT

14347.2

CTCCTCTTGGTACATGAACCCAAGTTGAAAGTGGACTTAACAAAGTATCTGGAGAACCAAGCATTCTGCTTTGACT
TTGCATTTGATGAAACAGCTTCGAATGAAGTTGTCTACAGGTTACAGCAAGGCCACTGGTACAGACAATCTTTGA
AGGTGGAAAAGCAACTTGTTTTGCATATGGCCAGACAGGAAGTGGCAAGACACATACTATGGGCGGAGACCTCTCT
GGGAAAGCCCAGAATGCATCCAAAGGGATCTATGCCATGGCCTTCCGGGACGTCTTCTTCTGAAGAATCAACCCTG
CTACCGGAAGTTGGGCCTGGAAGTCTATGTGACATTCTTCGAGATCTACAATGGGAAGCTGTTTGACCTGCTCAAC
AAGAAGGCCAAGCTTGCGCGTGCTGGAAGACGGCAAGCAACAGGTGCAAGTGGTGGGGGCTTGCAGGAACATCTGG
NTAACTCTGCTTGATGATGGCANTCAAGATGATCGACATGGGCAGCGCCTGCAGA

14348.2&14350.1&2

TCCCGAATTCAGCGACAAATTGGAWAGTGAAATGGAAGATGCCTATCATGAACATCAGGCAAATCTTTTGCGCCA
AGATCTGATGAGACGACAGGAAGAATTAAGACGCATGGAAGAACTTCACAATCAAGAAATGCAGAAACGTAAAGAA
ATGCAATTGAGGCAAGAGGAGGAACGACGTAGAAGAGAGGAAGAGATGATGATTCGTCAACGTGAGATGGAAGAAC
AAATGAGGCGCCAAAGAGAGGAAAGTTACAGCCGAATGGGCTACATGGATCCACGGGAAAGAGACATGCCAATGGG
TGGCGGAGGAGCAATGAACATGGGAGATCCCTATGGTTCAGGAGGCCAGAAATTTCCACCTCTAGGAGGTGGTGGT
GGCATAGGTTATGAAGCTAATCCTGGCGTTCCACCAGCAACCATGAGTGGTTCCATGATGGGAAGTGACATGCGTA
CTGAGCGCTTTGGGCAGGGAGGTGCGGGGCTGTGGGTGGACAGGGTCTAGAGGAATGGGGCTGGAACCTCCAGC
AGGATATGGTAGAGGGAGAGAAGAGTACGAAGGC

14349.1&2

TTCGTGAAGACCCTGACTGGTAAGACCATCACTCTCGAAGTGGAGCCCGAGTGACACCATTGAGAATGTCAAGGCA
AAGATCCAAGACAAGGAAGGCATCCCTCCTGACCAGCAKAGGTTGATCTTTGCTGGGAAACAGCTGGAAGATGGAC
GCACCCTGTCTGACTACAACATCCAGAAAGAGTCCACCCTGCACCTGGTGCTCCGTCTCAGAGGTGGGATGCAAAAT
CTTCGTGAAGACCCTGACTGGTAAGACCATCACCTCGAGGTGGAGCCCAGTGACACCATCGAGAATGTCAAGGCA
AAGATCCAAGATAAGGAAGGCATCCCTCCTGATCAGCAGAGGTTGATCTTTGCTGGGAAACAGCTGGAAGATGGAC
GCACCCTGTCTGACTACAACATCCAGAAAGAGTCCACTCTGCACTTGGTCTGCGCTTGAGGGGGGGTGTCTAAGT
TTCCCTTTTAAAGTTTCAACAAATTTCAATTGCACTTTCCTTTCAATAAAGTTGTTGCATTCT

Fig. 15R

14352.1&2

GCGCGGGTGCGTGGGCCACTGGGTGACCGACTTAGCCTGGCCAGACTCTCAGCACCTGGAAGCGCCCCGAGAGTGA
CAGCGTGAGGCTGGGAGGGAGGACTTGGCTTGAGCTTGTTAACTCTGCTCTGAGCCTCCTTGTCGCCTGCATTTA
GATGGCTCCCGCAAAGAAGGGTGGCGAGAAGAAAAAGGGCCGTTCTGCCATCAACGAAGTGGTAACCCGAGAATAC
ACCATCAACATTACAAGCGCATCCATGGAGTGGGCTTCAAGAAGCGTGCACCTCGGGCACTCAAAGAGATTGGGA
AATTTGCCATGAAGGAGATGGGAACTCCAGATGTGCGCATTGACACCAGGCTCAACAAAGCTGTCTGGGCCAAAGG
AATAAGGAATGTGCCATACCGAATCCGTGTGCGGCTGTCCAGAAAACGTAATGAGGATGAAGATTCACCAAATAAG
CTATATACTTTGGTTACCTATGTACCTGTTACCACTTTCAAAAATCTACAGACAGTCAATGTGGATGAGAACTAAT
CGCTGATCGT

14353.1

AATTCTTTATTTAAATCAACAACTCATCTTCTCAAGCCCCAGACCATGGTAGGCAGCCCTCCCTCTCCATCCCC
TCACCCACCCCTTAGCCACAGTGAAGGGAATGGAAAATGAGAAGCCACGAGGGCCCTGCCAGGGAAGGCTGCCC
CAGATGTGTGGTGAGCACAGTCAGTGCAGCTGTGGCTGGGGCAGCAGCTGCCACAGGCTCCTCCCTATAAATTAAG
TTCCTGCAGCCACAGCTGTGGGAGAAGCATACTTGTAGAAGCAAGGCCAGTCCAGCATCAGAAGGCAGAGGCAGCA
TCAGTGACTCCCAGCCATGGAATGAACGGAGGACACAGAGCTCAGAGACAGAACAGGCCAGGGGGAAGAAGGAGAG
ACAGAATAGGCCAGGGCATGGCGGTGAGGGA

14353.2

TGATGAATCTGGGTGGGCTGGCAGTAGCCCGAGATGATGGGCTCTTCTCTGGGGATCCCAACTGGTTCCTAAGAA
ATCCAAGGAGAATCTCGGAACTTCTCGGATAACCAGCTGCAAGAGGGCAAGAACGTGATCGGGTTACAGATGGGC
ACCAACCGCGGGGCGTCTCANGCAGGCATGACTGGCTACGGGATGCCACGCCAGATCCTCTGATCCCACCCAGGC
CTTGCCCTGCCCTCCACGAATGGTTAATATATATGTAGATATATATTTTAGCAGTGACATTCCCAGAGAGCCCC
AGAGCTCTCAAGCTCCTTTCTGTCAAGGTGGGGGTTCAAGCCTGTCTGTACCTCTGAAGTGCCTGCTGGCATC
CTCTCCCCCATGCTTACTAATAACATTCCCTTCCCCATAGCC

17182.1&2

AGCGGAGCTCCCTCCCCTGGTGGCTACAACCCACACACGCCAGGCTCAGGCATCGAGCAGAACTCCAGCGACTGGG
TAACCACTGACATTAGGTGAAGGTGCGGGACACCTACCTGGATACACAGGTGGTGGGACAGACAGGTGTCATCCG
CAGTGTACGGGGGGCATGTGCTCTGTGTACCTGAAGGACAGTGAGAAGGTTGTGAGCATTTCCAGTGAGCACCTG
GAGCCTATCACCCCAACAAGAACAAGGTGAAAGTGATCCTGGGCGAGGATCGGGAAGCCACGGGCGTCTTAC
TGAGCATTGATGGTGAGGATGGCATTGTCCGTATGGACCTTGATGAGCAGCTCAAGATCCTCAACCTCCGCTTCCT
GGGGAAGCTCCTGGAAGCCTGAAGCAGGCAGGGCCGGTGGACTTCGTGGATGAAGAGTGATCCTCCTTCCCTTCCC
TGGCCCTTGGCTGTGACACAAGATCCTCCTGCAGGGCTAGGCGGATTGTTCTGGATTTCTTTTGTCTTTTCTTTT
AGGTTTCCATCTTTTCCCTCCCTGGTGCTCATTGGAATCTGAGTAGAGTCTGGGGGAGGGTCCCCACCTTCTGTA
CCTCCTCCCCACAGCTTGCTTTTGTGTACCGTCTTCAATAAAAAGAAGCTGTTTGGTCTA

17183.2

GGTTCACAGCACTGCTGCTTGTGTGTTGCCGGCCAGGAATTCCAGGCTCACAAGGCTATCTTAGCAGCTCGTTCTC
CGGTTTTTTAGTGCCATGTTTGAACATGAAATGGAGGAGAGCAAAAAGAATCGAGTTGAAATCAATGATGTGGAGCC
TGAAGTTTTTAAGGAAATGATGTGCTTCATTTACACGGGGAAGGCTCCAAACCTCGACAAAATGGCTGATGATTTG
CTGGCAGCTGCTGACAAGTATGCCCTGGAGCGCTTAAAGGTCATGTGTGAGGATGCCCTCTGCAGTAACCTGTCCG
TGGAGAACGCTGCAGAAATTCATCCTGGCCGACCTCCACAGTGCAGATCAGTTGAAAACCTCAGGCAGTGATTT
CATCAACTATCATGCTTCGGATGTCTTGGAGACCTCTTGGG

17186.1&2

TCGTAGCCATTTTTCTGCTTCTTTGGAGAATGACGCCACACTGACTGCTCATTGTGCTTGGTTCCATGCCAATTGG
TGAAATAGAACCTCATCCGGTAGTGGAGCCGGAGGGACATCTTGTATCAACGGTGATGGTGCGATTTGGAGCATA
CCAGAGCTTGGTGTCTCGCCATACAGGGCAAAGAGGTTGTGACAAAGAGGAGAGATACGGCATGCCTGTGCAGCC
CTGATGCACAGTTCCTCTGCTGTGTACTCTCCACTGCCAGCCGGAGGGGCTCCCTGTCCGACAGATAGAAGATCA
CTTCCACCCCTGGCTTG

17187.1&2

TGGCACACTGCTCTTAAGAAACTATGAWGATCTGAGATTTTTTTGTGTATGTTTTTGA CTCTTTTGAGTGGTAATC
ATATGTGTCTTTATAGATGTACATACCTCCTTGACAAATGGAGGGGAATTCATTTTCATCACTGGGAGTGTCTT
AGTGTATAAAAACCATGCTGGTATATGGCTTCAAGTTGTAAAAATGAAAGTGACTTTAAAAGAAAATAGGGGATGG
TCCAGGATCTCCACTGATAAGACTGTTTTTAAGTAACTTAAGGACCTTTGGGTCTACAAGTATATGTGAAAAAAT
GAGACTTACTGGGTGAGGAAATTCATTGTTTAAAGATGGTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG
TTTTGTTTTTTAAGGGAGGGAATTTATTATTTACCGTTGCTTGAAATTACTGKGTAAATATATGTYTGATAATGAT
TTGCTYTTTGVMACCTAAAATTAGGVCTGTATAAGTWCTARATGCMTCCTGGGKGTGATYTTCCMAGATATTGA
TGATAMCCCTTAAAATTGTAACCYGCCTTTTCCCTTTGCTYTCMATTAAAGTCTATTCTMAAAG

17191.1&89.1

GGGGGTAGGCTCTTTATTAGACGGTTATTGCTGTACTACAGGGTCAGAGTGCAGTGTAAGCAGTGTGAGAGGCCCC
CGTTCAGCCCAAGAATGTGGATTTTCTCTCCCTATTGATCACAGTGGGTGGGTTTCTTCAGAAAAGCCCCAGAGGC
AGGGACCACTGAGCTCCAAGGTTAGAAGTGGAACTGGAAGGCTTCAGTCACATGCTGCTTCCACGCTTCCAGGCTG
GGCAGCAAGGAGGAGATGCCCATGACGTGCCAGGTCTCCCATCTGACACCAGTGAAGTCTGGTAGGACAGCAGCC
GCACGCCTGCCTCTGCCAGGAGGCCAATCATGGTAGGCAGCATTGCAGGGTCAGAGGTCTGAGTCCGGAATAGGAG
CAGGGGCAGGTCCCTGCGGAGAGGCACTTCTGGCCTGAAGACAGCTCCATTGAGCCCCTGCAGTACAGGYGTAGTG
CCTTGGACCAAGCCACAGCCTGGTAAGGGGCGCCTGCCAGGGCCACGGCCAGGAGGCA

17192.1&2

TAATTTCTTAGTCGTTTGAATCCTTAAGCATGCAAAAGCTTTGAACAGAAGGGTTCACAAAGGAACCAGGGTTGT
CTTATGGCATCCAGTTAAGCCAGAGCTGGGAATGCCTCTGGGTCATCCACATCAGGAGCAGAAGCACTTGACTTGT
CGGTCCTGCTGCCACGGTTTGGGCGCCACACGCCCACGTCCACCTCGTCCTCCCCTGCCGCCACGTCTGGGCG
GCCAAGGTCTCCAAAATTGATCTCCAGCTGAGACGTTATATCATTTGCTGGCTTCCGGAATGATGGTCCATAACC
GAATCTTCAGCATGAGCCTCTTCACTCTTTGATTTATGAAGAACAAATCCCTTCTTCCACTGCCCATCAGCACCTT
CATTTGGTTTTTCGGATATTAAATTCTACTTTTGCCCGTCTTATTTTGAATAGCCTTCCACTCATCCAAAGTCAT
CTCTTTTGGACCCTCCTCTTTTACCTCTTCAACTTCATTCTCCTTATTTTCAGTGTCTGCCACTGGATGATGTTCT
TCACCTTCAGGTGTTTCCTCAGTCACATTTGATTGATCCAAGTCAGTTAATTCGTCTTTGACAGTTCCCCAGTTGT
GAGATCCGCTACCTCCACGTTTGTCTCGTGCTTCAGGCCAGATCTACTTCCACTATGCCTATCAAATTCAGG
TTTGCCACGAGAATCAAATCCATCTCCTCGGCCATTCCACGTCCACGGCCCCCTCGACCTCTTCCAAGACCACCA
CGACCTCGAATAGGTCGGTCAATAATCGGTCTATCAACTGAAAATTCGCTCCTTACCCTTTTCTTCAAGTGGCT
TTTCGAATCTTCGTTACGAGGTGGTCGCCTTTCTGGTCTTCTATCAATTATTTTCCCTTACCCTGAAGTTGTTG
ATCAGGTCTTCTTCCAACCTCGTGC

17193

AAGCGGATGGACCTGAGTCAGCCGAATCCTAGCCCCCTTCCCTTGGGCCTGCTGTGGTGCTCGACATCAGTGACAGA
CGGAAGCAGCAGACCATCAAGGCTACGGGAGGCCCGGGCGCTTGCGAAGATGAAGTTTGGCTGCCTCTCCTTCCG
GCAGCCTTATGCTGGCTTTGTCTTAAATGGAATCAAGACTGTGGAGACGCGCTGGCGTCTCTGCTGAGCAGCCAG
CGGAAGTGTACCATCGCCGTCCACATTGCTCAGGGGACTGGGAAGGCGATGCCTGTGCGGGAGCTGCTGGTGGAGA
GACTCGGGATGACTCCTGCTCAGATTCAAGCCTTGCTCAGGAAAGGGGAAAAGTTTGGTCGAGGAGTGATAGCGGG
ACTCGTTGACATTGGGGAAACTTTGCAATGCCCCGAAGACTTAACTCCCGATGAGGTTGTGGAACTAGAAAATCAA
GCTGCACTGACCAACCTGAAGCAGAAGTACCTGACTGTGATTTCAAACCCCAGGTGGTTACTGGAGCCCATACCTA
GGAAAGGAGGCAAGGATGTATTCCAGGTAGACATCCAGAGCACCTGATCCCTTTGGGGCATGAAGTGTGACAAGT
GTGGGCTCCTGAAAGGAATGTTCCRGAGAAACCAGCTAAATCATGGCACCTTCAATTTGCCATCGTGACGCAGACC
TGTATAAATTAGGTTAAAGATGAATTTCCACTGCTTTGGAGAGTCCCACCCACTAAGCACTGTGCATGTAAACAGG
TTCCTTTGCTCAGATGAAGGAAGTAGGGGTGGGGCTTTCTTGTGTGATGCCTCCTTAGGCACACAGGCAATGTC
TCAAGTACTTTGACCTTAGGGTAGAAGGCAAAGCTGCCAGTAAATGTCTCAGCATTGCTGCTAATTTTGGTCTGC
TAGTTTCTGGATTGTACAAATAAATGTGTTGTAGATGA

Fig. 15U

16443.1.edit

TCGAGCGGCCCGCCGGGCAGGTGTCGGAGTCCAGCACGGGAGGCGTGGTCTTGTAGTTGTTCTCCGGCTGCCATT
GCTCTCCCACTCCACGGCGATGTCGCTGGGATAGAAGCCTTTGACCAGGCAGGTGAGGCTGACCTGGTTCTTGGTC
ATCTCCTCCCGGGATGGGGGCAGGGTGTACACCTGTGGTTCTCGGGGCTGCCCTTTGGCTTTGGAGATGGTTTTCT
CGATGGGGGCTGGGAGGGCTTTGTTGGAGACCTTGCACTTGTACTCCTTGCCATTCAACCAGTCCTGGTGCANGAC
GGTGAGGACGCTNACCACACGGTACGNGCTGGTGTACTGCTCCTCCCGCGGCTTTGTCTTGGCATTATGCACCTCC
ACGCCGTCCACGTACCAATTGAACTTGACCTCAGGGTCTTCGTGGCTCACGTCCACCACCACGCATGTAACCTCAA
ANCTCGGNCGCGANACGC

16443.2.edit

AGCGTGGTCGCGGCCGAGGTCTGAGGTTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTC
AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACC
GTGTGGTCAGCGTCCTCACCCTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGAAGGTCTCCAACAA
AGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCTG
CCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTGAGCTGACCTGCCTGGTCAAAGGCTTCTATCCAGCGACA
TCGCCCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACCTACAAGACCACGCCTCCCGTGCTGGACTCCGACA
CCTGCCGGGCGGCCGCTCGA

16444.2.edit

AGCGTGGTTNCGGCCGAGGTCCCAACCAAGGCTGCANCCTGGATGCCATCAAAGTCTTCTGCAACATGGAGACTGG
TGAGACCTGCGTGTACCCCACTCAGCCAGTGTGGCCAGAAGAAGTGGTACATCAGCAAGAACCCCAAGGACAAG
AGGCATGTCTGGTTCGGCGAGAGCATGACCGATGGATTCCAGTTCGAGTATGGCGGCCAGGGCTCCGACCCTGCCG
ATGTGGACCTGCCCCGGGCGGNCGCTCGA

16445.1.edit

AGCGTGGTCGCGGCCGAGGTCAAGAACCCCGCCCGCACCTGCCGTGACCTCAAGATGTGCCACTCTGACTGGAAGA
GTGGAGAGTACTGGATTGACCCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGGAGACTGG
TGAGACCTGCGTGTACCCCACTCAGCCAGTGTGGCCAGAAGAAGTGGTACATCAGCAAGAACCCCAAGGACAAG
AGGCATGTCTGGTTCGGCGAGAGCATGACCGATGGATTCCAGTTCGAGTATGGCGGCCAGGGCTCCGACCCTGCCG
ATGTGGACCTGCCCCGGGCGGCCGCTCGA

16445.2.edit

TCGAGCGGTCGCCCCGGGCAGGTCCACATCGGCAGGGTCGGAGCCCTGGCCGCCATACTCGAACTGGAATCCATCGG
NCATGCTCTCGCCGAACCAGACATGCCTCTTGNCCTTGGGGTTCTTGCTGATGTACCAGNTCTTCTGGGCCACACT
GGGCTGAGTGGGGTACACGCAGGTCTCACCANTCTCCATGTTGCANAAGACTTTGATGGCATCCAGGTTGCAGCCT
TGGTTGGGGTCAATCCAGTACTCTCCACTCTTCCAGACAGAGTGGCACATCTTGAGGTACGGCAGGTGCGGGCGG
GGTTCTTGACCTCGGTGCGGACCACGCT

16446.1.edit

TCGAGCGGCCGCCCCGGGCAGGTCCCTCCTCAGAGCGGTAGCTGTTCTTATTGCCCCGGCAGCCTCCATAGATNAAGT
TATTGCANGAGTTCCTCTCCACGTCAAAGTACCAGCGTGGGAAGGATGCACGGCAAGGCCAGTGACTGCGTTGGC
GGTGCAGTATTCTTCATAGTTGAACATATCGCTGGAGTGGACTTCAGAATCCTGCCTTCTGGGAGCACTTGGGACA
GAGGAATCCGCTGCATTCTGCTGGTGGACCTCGGCCGCGACCACGCT

16446.2.edit

AGCGTGGTCGCGGCCGAGGTCCACCAGCAGGAATGCAGCGGATTCTCTGTCCCAAGTGCTCCCAGAAGGCAGGAT
TCTGAAGACCACTCCAGCGATATGTTCAACTATGAAGAATACTGCACCGCCAACGCAGTCACTGGGCCTTGCCGTG
CATCCTTCCACGCTGGTACTTTGACGTGGAGAGGAACCTCTGCAATAACTTCATCTATGGAGGCTGCCGGGGCAA
TAAGAACAGCTACCGCTCTGAGGAGGACCTGCCCGGGCGGCCGCTCGA

16447.1.edit

TCGAGCGGCCGCCCCGGGCAGGTCCACATCGGCAGGGTCGGAGCCCTGGCCGCCATACTCGAACTGGAATCCATCGG
TCATGCTCTCGCCGAACCAGACATGCCTCTTGTCCTTGGGGTTCTTGCTGATGTACCAGTTCTTCTGGGCCACACT
GGGCTGAGTGGGGTACACGCAGGTCTCACCAGTCTCCATGTTGCAGAAGACTTTGATGGCATCCAGGTTGCAGCCT
TGGTTGGGGTCAATCCAGTACTCTCCACTCTTCCAGCCAGAATGGCACATCTTGAGGTACGGCANGTGCGGGCGG
GGTTCTTGACCTCGGCCGCGACCACGCT

16447.2.edit

AGCGTGGTCGCGGCCGAGGTCAAGAAACCCCGCCCGCACCTGCCGTGACCTCAAGATGTGCCACTCTGGCTGGAAG
AGTGGAGAGTACTGGATTGACCCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGGAGACTG
GTGAGACCTGCGTGTACCCCACTCAGCCAGTGTGGCCCAAGAAGTGGTACATCAGCAAGAACCCCAAGGACAA
GAGGCATGTCTGGCTCGGCGAGAGCATGACCGATGGATTCCAGTTCGAGTATGGCGGCCAGGGCTCCGACCCTGCC
GATGTGGACCTGCCCGGGCGGCCGCTCGA

16449.1.edit

AGCGTGGTCGCGGCCGAGGTCCTGTCAGAGTGGCACTGGTAGAAGNTCCAGGAACCCTGAACTGTAAGGGTTCTTC
ATCAGTGCCAACAGGATGACATGAAATGATGTACTCAGAAGTGTCTGNAATGGGGCCCATGANATGGTTGNCTGA
GAGAGAGCTTCTTGTCTACATTGGCGGGTATGGTCTTGGCCTATGCCTTATGGGGGTGGCCGTTGNGGGCGGTG
NGGTCCGCCTAAAACCATGTTCTCAAAGATCATTTGTTGCCCAACACTGGGTTGCTGACCANAAGTGCCAGGAAG
CTGAATACCATTTCCAGTGTACATCCAGGGTGGGTGACGAAAGGGGTCTTTTGAAGTGTGGAAGGAACATCCAAG
ATCTCTGNTCCATGAAGATTGGGGTGTGGAAGGGTTACCAGTTGGGGAAGCTCGCTGTCTTTTCTTCCAATCAN
GGGCTCGCTCTTCTGAATATTCTTCAGGGCAATGACATAAATTGTATATTCGGTTCCTGGTTCAGGCCAG

16450.1.edit

TCGAGCGGCCGCGCGGGCAGGTCCACCACACCCAATTCTTGCTGGTATCATGGCAGCCGCCACGTGCCAGGATTA
CCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGTGGTCCCTCGGCCCCGCCCTGGTGTAC
AGAGGCTACTATTACTGGCCTGGAACCGGGAACCGAATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAG
AGCGAGCCCCTGATTGGAAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCTTCACACCCCAATCTTCATG
GACCAGAGATCTTGGATGTTCTTCCACAGTTCAAAAGACCCCTTTTCGTACCCACCCTGGGTATGACACTGGAAA
TGGTATTCAGCTTCTTGGCACTTCTGGTCAGCAACCCAGTGTGGGCAACAAATGATCTTTGANGAACATGGNTTT
AGGCGGACCACACCGGCCACAACGGGCACCCCATTAAGGCATAGGCCAAGAACATACCCGNCGAATGTAGGACAAG
AAGCTCTNTCTCANACAANCATCTCATGGGCCCCATTCCANGACACTTCTGAGTACATCANTTCATGGCATCCTGG
TGGCACTGATAAAAACCTTACAGTTA

16450.2.edit

AGCGTGGTCGCGGGCGAGGTCCTGTCAGAGTGGCACTGGTAGAAGTTCCAGGAACCCTGAACTGTAAGGGTTCTTC
ATCAGTGCCAACAGGATGACATGAAATGATGTACTCAGAAGTGTCTGGAATGGGGCCCATGAGATGGTTGTCTGA
GAGAGAGCTTCTTGTCTACATTGGCGGGTATGGTCTTGGCCTATGCCTTATGGGGGTGGCCGTTGTGGGCGGTG
TGGTCCGCCTAAAACCATGTTCTCAAAGATCATTTGTTGCCCAACACTGGGTTGCTGACCAGAAGTGCCAGGAAG
CTGAATACCATTTCCAGTGTACATCCAGGGTGGGTGACGAAAGGGGTCTTTTGAAGTGTGGAAGGAACATCCAAG
ATCTCTGGTCCATGAAGATTGGGGTGTGGAAGGGTTACCAGTTGGGGAAGCTCGTCTGTCTTTTCTTCCAATCA
NNGGCTCGCTCTTCTGATTATTCTTCAGGGCAATGACATAAATTGTATATTCGGNTCCCGGGTNCAGCCAATAATA
ATAACCCTCTGTGACACCANGGCGGGGCCGAAGGANCAT

16451.1.edit

AGCGTGGTCGCGGCCGAGGTCCTCACCAGAGGTACCACCTACAACATCATAGTGGAGGCACTGAAAGACCAGCAGA
GGCATAAGGTTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTTGAACCAACCTACGGATGACTC
GTGCTTTGACCCCTACACAGTTTCCATTATGCCGTTGGAGATGAGTGGGAACGAATGTCTGAATCAGGCTTTAAA
CTGTTGTGCCAGTGCTTANGCTTTGGAAGTGGTCATTTTCAGATGTGATTCATCTAGATGGTGCCATGACAATGGTG
TGAACTACAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGACCTGCCCGGGCGGCCGCTCGA

16451.2.edit

TCGAGCGGCCGCCCCGGGCAGGTCCATTTCTCCCTGACGGTCCCACTTCTCTCCAATCTTGTAGTTCACACCATTG
TCATGGCACCATCTAGATGAATCACATCTGAAATGACCACTTCCAAAGCCTAAGCACTGGCACAACAGTTTAAAGC
CTGATTCAGACATTCGTTCCCACTCATCTCCAACGGCATAATGGGAACTGTGTAGGGGTCAAAGCACGAGTCATC
CGTAGGTTGGTTCAAGCCTTCGNTGACAGAGTTGCCACGGTAACAACCTCTTCCCGAACCTTATGCCTCTGCTGG
TCTTTCAGTGCCTCCACTATGATGTTGTAGGTGGTACCTCTGGTGAGGACCTCGGCCGCGACCACGCT

16452.1.edit

AGCGTGGCCGCGGCCGAGGTCCATTGGCTGGAACGGCATCAACTTGGAAGCCAGTGATCGTCTCAGCCTTGGTTCT
CCAGCTAATGGTGATGGNGGTCTCAGTAGCATCTGTACACAGAGCCCTTCTTGGTGGGCTGACATTCTCCAGAGTG
GTGACAACACCCTGAGCTGGTCTGCTTGTCAAAGTGTCTTAAGAGCATAGACACTCACTTCATATTTGGCGNCCA
CCATAAGTCCTGATACAACCACGGAATGACCTGTCAGGAAC

16452.2.edit

TCGAGCGGCCGCCCCGGGCAGGTCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGATGATAT
GGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCTGCACCAACTGACCTGAAGTTCACTCAGGTCACA
CCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGTTTCAGCTCACTGGATATCGAGTGCGGGTGACCCCAAGG
AGAAGACCGGACCAATGAAAGAAATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGCGGC
CACCAAATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGTGTGTACCACT
CTGGAGAATGTCAGCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGAGACCACCATCACCATTAGCTGGAGAA
CCAAGACTGAGACGATCACTGGCTTCCAAGTTGATGCCGTTCCAGCCAATGGACCTCGGCCGCGACCACGCTT

16453.1.edit

AGCGTGGTCGCGGCCGAGGTCTGGCCGAAGTCCAGTGTACAGGGAAGATGTACATGTTATAGNTCTTCTCGAAGT
CCCGGGCCAGCAGCTCCACGGGGTGGTCTCCTGCCTCCAGGCGTTCTCATTCTCATGGATCTTCTTCACCCGCAG
CTTCTGCTTCTCAGTCAGAAGGTTGTTGTCTCATCCCTCTCATACAGGGTGACCAGGACGTTCTTGAGCCAGTCC
CGCATGCGCAGGGGGAATTCGGTCAGCTCAGAGTCCAGGCAAGGGGGGATGTATTTGCAAGGCCCGATGTAGTCCA
AGTGGAGCTTGTGGCCCTTCTTGGTGCCCTCCAAGGTGCACTTTGTGGCAAAGAAGTGGCAGGAAGAGTCGAAGGT
CTTGTTGTATTGCTGCACACCTTCTCAAACCTGCCAATGGGGGCTGGGCAGACCTGCCCCGGCGGCCGCTCGA

16453.2.edit

TCGAGCGGCCCGCCGGGCAGGTCTGCCAGCCCCCATTGGCGAGTTTGAGAAGGNGTGCAGCAATGACAACAAGAC
CTTCGACTCTTCTGCCACTTCTTTGCCACAAAGTGACCCCTGGAGGGCACCAAGAAGGGCCACAAGCTCCACCTG
GACTACATCGGGCCTTGCAAATACATCCCCCTTGCCTGGACTCTGAGCTGACCGAATTCCTGCGCATGCGGG
ACTGGCTCAAGAACGTCTGGTCACCCTGTATGAGAGGGATGAGGACAACAACCTTCTGACTGAGAAGCANAAGCT
GCGGGTGAAGAANATCCATGAGAATGANAAGCGCCTGNAGGCANGAGACCACCCGTTGGAGCTGCTGGCCCCGGGAC
TTCGAGAAGAACTATAACATGTACATCTTCCCTGTACACTGGCAGTTCGGCCAGACCTCGGCCGCGACCACGCT

16454.1.edit

AGCGTGGNTGCGGACGACGCCCCACAAAGCCATTGTATGTAGTTTTANTTCAGCTGCAAANAATACCNCCAGCATCC
ACCTTACTAACCAGCATATGCAGACA

16454.2.edit

TCGAGCGGTGCGCCGGGCAGGTCTGGGCGGATAGCACCGGGCATATTTTGAATGGATGAGGTCTGGCACCCCTGAG
CAGCCCAGCGAGGACTTGGTCTTAGTTGAGCAATTTGGCTAGGAGGATAGTATGCAGCACGGTTCTGAGTCTGTGG
GATAGCTGCCATGAAGNAACCTGAAGGAGGCGCTGGCTGGTANGGGTTGATTACAGGGCTGGGAACAGCTCGTACA
CTTGCCATTCTCTGCATATACTGGNTAGTGAGGCGAGCCTGGCGCTCTTCTTTGCGCTGAGCTAAAGCTACATACA
ATGGCTTTGNGGACCTCGGCCGCGACCACGCTT

16455.1.edit

TCGAGCGGCCGCCCCGGGCAGGTCCATTTCTCCCTGACGGTCCCACTTCTCTCCAATCTTGTAGTTCACACCATTG
TCATGACACCATCTAGATGAATCACATCTGAAATGACCACTTCCAAAGCCTAAGCACTGGCACAACAGTTTAAAGC
CTGATTCAGACATTCGTTCCCACTCATCTCCAACGGCATAATGGGAACTGTGTAGGGGTCAAAGCACGAGTCATC
CGTAGGTTGGTTCAAGCCTTCGTTGACAGAAGTTGCCACGGTAACAACCTCTTCCCGAACCTTATGCCTCTGCTG
GTCTTTCAAGTGCCTCCACTATGATGTTGTAGGTGGCACCTCTGGTGAGGACCTCGGCCGCGACCACGCT

16455.2.edit

AGCGTGGTTTGC GGCCGAGGTCTCACCANAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCAGCAG
AGGCATAAGGTTCCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTTGAACCAACCTACGGATGACT
CGTGCTTTGACCCCTACACAGNTTCCATTATGCCGTTGGAGATGAGTGGGAACGAATGTCTGAATCAGGCTTTAA
ACTGTTGTGCCAGTGCTTANGCTTTGGAAGTGGTCATTTAGATGTGATTCATCTANATGGTGTGATGACAATGGT
GNGAACTACAAGATTGGAGAGAAGTGGNACCGTCAGGGGANAAAATGGACCTGCCCGGGCGGCNCGCTCGA

16456.1.edit

AGCGTGGTCGCGGCCGAGGTCTGGCTTNCTGCTCANGTGATTATCCTGAACCATCCAGGCCAAATAAGCGCCGGCT
ATGCCCCTGNATTGGATTGCCACACGGCTCACATTGCATGCAAGTTTGCTGAGCTGAAGGAAAAGATTGATC

16456.2.edit

TCGAGCGGCCGCCCCGGGCAGGTCCAATTGAAACAAACAGTTCTGAGACCGTTCTTCCACCACTGATTAAGAGTGGG
GNGGCGGGTATTAGGGATAATATTCATTTAGCCTTCTGAGCTTTCTGGGCAGACTTGGTGACCTTGCCAGCTCCAG
CAGCCTTCTGGTCCACTGCTTTGATGACACCCACCGCAACTGTCTGTCTCATATCACGAACAGCAAAGCGACCCAA
AGGTGGATAGTCTGAGAAGCTCTCAACACACATGGGCTTGCCAGGAACCATATCAACAATGGGCAGCATCACCAGA
CTTCAAGAATTTAAGGGCCATCTTCCAGCTTTTTACCAGAACGGCGATCAATCTTTTCTTCAGCTCAGCAAACCTT
GCATGCAATGTGAGCCG

Fig. 15AA

16459.1.edit

TCGAGCGGCCCGCCGGGCAGGTCCAGAGGGCTGTGCTGAAGTTTGCTGCTGCCACTGGAGCCACTCCAATTGCTGG
CCGCTTCACTCCTGGAACCTTCACTAACCAGATCCAGGCAGCCTTCCGGGAGCCACGGCTTCTTGTTGGNTACTGAC
CCCAGGGCTGACCACCAGCCTCTCACGGAGGCATCTTATGTTAACCTACCTACCATTGCGCTGTGTAACACAGATT
CTCCTCTGCGCTATGTGGACATTGCCATCCCATGCAACAACAAGGGAGCTCACTCAGNGGGGTTTGATGTGGTGGG
TGCTGGCTCGGGAAGTTCTGCGCATGCGTGGCACCATTTCCTGTAACACCCATGGGANGNCATGCCTGATCTGGA
CTTCTACAGAGATCCTGAAGAGATTGAAAAAGAAGAACAGGCTGNTTGCTGANAAAGCAAGTGACCAAGGANGAAA
TTTCANGGGTGAAANGGACTGCTCCCGCTCCTGAATTCAGTCTACTCAACCTGANGNTGCAGACTGGTCTTGAAG
GNGNACANGGGCCCTCTGGGCCTATTTAAGCANCTTCGGTCGCGAACACGNT

16459.2.edit

AGCGTGNGTCGCGGCCGAGGTGCTGAATAGGCACAGAGGGCACCTGTACACCTTCAGACCAGTCTGCAACCTCAGG
CTGAGTAGCAGTGAACCTCAGGAGCGGGAGCAGTCCATTACCCTGAAATTCCTCCTTGGNCACTGCCTTCTCAGCA
GCAGCCTGCTCTTCTTTTTCAATCTCTTCAGGATCTCTGTAGAAGTACAGATCAGGCATGACCTCCCATGGGTGTT
CACGGGAAATGGTGCCACGCATGCGCAGAACTTCCCGAGCCAGCATCCACCACATCAAACCCACTGAGTGAGCTCC
CTTGTTGTTGCATGGGATGGGCAATGTCCACATAGCGCAGAGGAGAATCTGTGTTACACAGCGCAATGGTAGGTAG
GTTAACATAAGATGCCTCCGCGAGAAGCTGGTGGTCAGCCCTGGGGTCAAGTAACCACAAGAAGCCGTGGCTCCCG
GAAGGCTGCCTGGATCTGGTTAGTGAAGGNTCCAGGAGTGAAGCGGCCAACAAATTGGAGTGGCTTCAGTGGCAAGC
AGCAAACCTCAGCACAAAGCCCTCTGGACCTGCCCCGGCGGCCGCTCGA

16460.1.edit

TCGAGCGGCCCGCCGGGCAGGTCCATTTCTCCCTGACGGNCCCACTTCTCTCCAATCTTGTTAGTTTACACCATTG
TCATGGCACCATCTAGATGAATCACATCTGAAATGACCACTTCCAAAGCCTAAGCACTGGCACAACAGTTTAAAGC
CTGATTCAGACATTCGTTCCCACTCATCTCCAACGGCATAATGGGAACTGTGTAGGGGTCAAAGCACGAGTCATC
CGTAGGTTGGTTCAAGCCTTCGTTGACAGAGTTGCCACGGTAACAACCTCNTCCCCGAACCTTATGCCTCTGCTG
GGCTTTCAGNGCCTCCACTATGATGNTGTAGGGGGGCACCTCTGGNGANGACCTCGGCCGCGACCACGCT

16460.2.edit

AGCGTGGTCGCGGCCGAGGTCCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCAGCAGA
GGCATAAGGCTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTTGAACCAACCTACGGATGACTC
GTGCTTTGACCCCTACACAGTTTCCATTATGCCGTTGGAGATGAGTGGGAACGAATGTCTGAATCAGGCTTTAAA
CTGTTGTGCCAGTGCTTANGCTTTGGAAGTGGGTCAATTCAGATGTGATTCATCTAGATGGTGCCATGACAATGGN
GNGAACTACAAGATTGGAGAGAAGTGGNACCGNCAGGGAGAAAATGGACCTGCCCGGGCGGCCGCTCGA

Fig. 15BB

16461.1.edit

AGCGTGGTCGCGGCCGAGGTCCACATCGGCAGGGTCGGAGCCCTGGCCGCCATACTCGAACTGGAATCCATCGGTC
ATGCTCTCGCCGAACCAGACATGCCTCTTGTCCTTGGGGTCTTGCTGATGTACCAGTTCTTCTGGGCCACACTGG
GCTGAGTGGGGTACACGCAGGTCTCACCAGTCTCCATGTTGCAGAAGACTTTGATGGCATCCAGGNTGCAACCTTG
GTTGGGGTCAATCCAGTACTCTCCACTCTTCCAGCCAGAGTGGCACATCTTGAGGTACGGCAGGTGCGGNCGGGG
GNTTTTGGGCTGCCCTCTGGNCTTCGGNTGTNCTCNATCTGCTGGCTCA

16461.2.edit

TCGAGCGGCCGCCCCGGGCAGGTCTCGCGGTGCACTGGTGATGCTGGTCCTGTTGGTCCCCCGGCCCTCCTGGAC
CTCCTGGCCCCCTGGTCCTCCCAGCGCTGGTTTTGACTTCAGCTTCCTGCCCCAGCCACCTCAAGAGAAGGCTCA
CGATGGTGGCCGCTACTACCGGGCTGATGATGCCAATGTGGTTCGTGACCGTGACCTCGAGGTGGACACCACCTC
AAGAGCCTGAGCCAGCAGATCGAGAACATCCGGAGCCCAGAGGGCAGNCGCAAGAACCCCGCCCGCACCTGCCGTG
ACCTCAAGATGTGCCACTCTGACTGGAAGAGTGGAGAGTACTGGATTGACCCCAACCAAGCTGCAACCTGGATGCC
ATCAAAGTCTTCTGCAACATGGAGACTGGTGAGACCTGCGTGTACCCCACTCAGCCAGTGTGGCCAAAAGAAGT
GGTACATCAGCAAGAACCCCAAGGACAAGAAGCATGTCTGGTTCGGCGAGAACATGACCGATGGATTCCAGTTCGA
GTATGGCGGGCAGGGCTCCGACCCTGCCGATGGGGACCTTGGCCGCGAACACGCT

16463.1.edit

AGCGTGGNNGCGGCCGAGGTATAAATATCCAGNCCATATCCTCCCTCCACACGCTGANAGATGAAGCTGTNCAAAG
ATCTCAGGGTGGANAAAACCAT

16463.2.edit

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ACGGCCTGTTGTGGGACAGTCTCTGTAATCGCGAAAGCAACCATGGAAGACCTGGGGGAAAACACCATGGTTTTAT
CCACCCTGAGATCTTTGAACAACTTCATCTCTCAGCGTGGGAGGGAGGCTCTGGACTGGATATTTCTACCTCGGC
CGGACACGCT

16464.1.edit

CGAGCGGGCGACCGGGCAGGTNCAGACTCCAATCCANANAACCATCAAGCCAGATGTCAGAAGCTACACCATCACA
GGTTTACAACCAGGCACTGACTACAAGANCTACCTGCACACCTTGAATGACAATGCTCGGAGCTCCCCTGTGGTCA
TCGACGCCTCCACTGCCATTGATGCACCATCCAACCTGCGTTTCTGGCCACCACACCAATTCCTTGCTGGTATC
ATGGCAGCCGCCACGTGCCAGGATTACCGGTACATCATNAGTATGANAAGCCTGGGCCTCCTCCCAGAGAAGNGG
TCCCTCGGCCCCGCCCTGNTGTCCANAGGNTACTATTACTGNGCCNGCAACCGGCAACCGATATCNATTTTGNCA
TTGGCCTTCAACAATAATTA

16464.2.edit

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AGAGAGAGCTTCTTGNCTGTCTTTTTCTTCCAATCAGGGGCTCGCTCTTCTGATTATTCTTCAGGGCAATGACA
TAAATTGTATATTGCGGTCCCGNTCCAGGCCAGTAATAGTANCCTCTGTGACACCAGGGCGGNGCCGAGGGACCA
CTTCTCTGGGAGGAGACCCAGGCTTCTCATACTTGATGATGTAACCGGTAATCCTGGCACGTGGCGGCTGCCATGA
TACCAGCAAGGAATTGGGTGTGGTGGCCAGGAAACGCAGGTTGGATGGNGCATCAATGGCAGTGGAGGCCGTGCA
TGACCACAGGGGGAGCTCCGACATTGTCATTCAAGGTG

16465.1.edit

AGCGTGGNCGCGGCCGAGGTGCAGCGCGGGCTGTGCCACCTTCTGCTCTCTGCCCAACGATAAGGAGGGTNCCTGC
CCCCAGGAGAACATTAACNTCCCCAGCTCGGCCTCTGCCGG

16465.2.edit

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CCATTGCGGCGGCATTTTCATCTGGCCAGGACACTGGCTGTCCACCTGGCACTGGTCCCGACAGAAGCCCCGAGCTGG
GGAAAGTTAATGTTACCTGGGGGCAGGAACCCCTCCTTATCATTGNGCAGAGAGCAGAAGGTGGCACAGCCCGCGC
TGCACCTCGGCCGCGACACGCT

16466.2.edit

TCGAGCGGCCCGCCCGGGCAGGTCCACCATAAGTCCTGATACAACCACGGATGAGCTGTCAGGAGCAAGGTTGATTT
CTTTCATTGGTCCGGNCTTCTCCTTGGGGGNCACCCGCACTCGATATCCAGTGAGCTGAACATTGGGTGGCGTCCA
CTGGGCGCTCAGGCT

16467.2.edit

TCGAGCGGTTGCCCCGGGCAGGTCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACGTGCCAGGATT
ACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGCGGTCCCTCGGCCCCGCCCTGGTGTCA
CAGAGGCTACTATTACTGGCCTGGAACCGGGAACCGAATATACAATTTATGTCATTGNCCTGAAGAATAATCANNA
ANAGCGANCCCTGATTGGAAGGA

Fig. 15DD

Fig. 15EE

06_16471.edit

AGCGTGGTCGCGGCCGAGGTCTGCTGCTTCAGCGAAGGGTTTCTGGCATAACCAATGATAAGGCTGCCAAAGACTG
TTCCAATACCAGCACCAGAACCAGCCACTCCTACTGTTGCAGCACCTGCACCAATAAATTTGGCAGCAGTATCAAT
GTCTCTGCTGATTGCACTGGTCTGAAACTCCCTTTGGATTAGCTGAGACACACCATTCTGGGCCCTGATTTTCCTA
AGATAGAACTCCAACCTCTTTGCCCTCTAGCACATAGCCATCTGCTCGGTCACACTGTCCCGGCCCTGAAGCGATGC
ACGCAAGAAGCTTGCCCTGCTGGAAGTCTCCTCCAGGAGACTGCTGATTTTGGCATTCTTTTTCTTTTCATCATA
TTTTCTTCTGAATTTTTTTAGATCGTTTTTTGTTTAAATCTCTTCTTCTCAGGAGTCAGCTTGGCCCCCGCCGCA
TCCACACAGTCCGTGTGCGGGGAGGTAACAAGAAATACCGTGCCCTGAGGTTGGACGTGGGGAATTTCTCCTGGGG
CTCAGAGTGGTGTACTCGTAAACAAGGATCATCGATGGTGNCTACAATGCATCTAATAACGAGCTGGGTGGGACC
CAAAGAACCTGGNGAANAATGGATCGNCTCATCGACAGGACACCGTACCCGACAGGGGNACGANTCCCACTATGC
GCTTGCCCTGGGGCCGAANAAGGAAAAGTGCCTGGGCGGCCNTCGAAAGCCCAATTNTGGAAAAATCCATCAC
ACTGGGNGGCCNGTCGAGCATGCATNTANAGGGGCCCATTCCTCCCTNANN

07_16472.edit

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TGGTGAGACCTGCGTGTACCCCACTCAGCCAGTGTGGCCCAGAAGAACTGGTACATCAGCAAGAACCCCAAGGAC
AAGAGGCATGTCTGGTTCGGCGAGAGCATGACCGATGGATTCCAGTTCGAGTATGGCGGCCAGGGCTCCGACCCTG
CCGATGTGGACCTCGGCCGCGACACGCT

08_16472.edit

AGCGTGGTCGCGGCCGAGGTCCACATCGGCAGGGTCGGAGCCCTGGCCGCCATACTCGAACTGGAATCCATCGGTC
ATGCTCTCGCCGAACCAGACATGCCTCTTGTCTTGGGGTTCTTGCTGATGTACCAGTTCTTCTGGGCCACACTGG
GCTGAGTGGGGTACACGCAGGTCTCACCAGTCTCCATGTTGCAGAAGACTTTGATGGCATCCAGGTTGCAGCCTTG
GTTGGGGACCTGCCCCGGGCGGCCGCTCGA

09_16473.edit

TCGAGCGGCCGCCCCGGGCAGGTCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACGTGCCAGGATTA
CCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGTGGTCCCTCGGCCCGCCCTGGTGTAC
AGAGGCTACTATTACTGGCCTGGAACCGGAACCGAATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAG
AGCGAGCCCTGATTGGAAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCTTCCACACCCCAATCTTCATG
GACCAGAGATCTTGGATGTTCTTCCACAGTTCAAAGACCCCTTTCGTCACCCACCCTGGGTATGACACTGGAAA
TGGTATTAGCTTCTTGGCACTTCTGGTCAGCAACCCAGTGTGGGCAACAAATGATCTTTGAGGAACATGGNTTT
AGGCGGACCACACCGCCACAACGGCCACCCCATAGGCAAGACCATAACCGCCGAATGTAGGACAAG
AAGCTNTNTNACANACACCATNTNATGGGCCCCATTCCAGGACACTTCTGAGTACATCATTTATGNCATCTGTGGC
ACTTGATGAAAACCTTACAGTTCAGGGTCTGGAACTTTTACCAGGCCTNTTACAGGACTNGGCCGGACNCCTTA
AGCCNATTNACCCCTGGGGCGTTCTANGGTCCCACTCGNNCACTGGNGAAAATGGCTACTGTN

11_16474.edit

AGCGTGGTCGCGGCCGAGGTCCACTAGAGGTCTGTGTGCCATTGCCAGGCAGAGTCTCTGCGTTACAAACTCCTA
GGAGGGCTTGCTGTGCGGAGGGCCTGCTATGGTGTGCTGCGGTTTCATCATGGAGAGTGGGGCCAAAGGCTGCGAGG
TTGTGGTGTCTGNAAACTCCNAGGACANGAGGGCTAAATTCATGAAGTTTGTGGATGGCCTGATGATCCACAAT
CGGAGACCCTGTAACTACTACCGTCTNACCNCCTGCTGTNCNCCCCNTTCTGCTNAANACATNGGGNTNNTNC
TTGNCCNTCCTTGGGTNGAANATNNAATNGCCTNCCNTTTCNTANCNCTACTNGNTCCANANTTGGCCTTTAAANA
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CCCCCTCCTCATTNANCCNATANGCTNNNAANTCCTTNANNCCTCCNCCCNTNCNCTCNTACTNANTNCTTCTN
NCCCATTACNNAGCTCTTTCNTTTAANATAATGNNGCCNNGCTCTNCATNTCTACNATNTGNNAATNCCCCCNCC
CCCNANCGNNTTTTTGACCTNNNAACCTCCTTCTCCTTCCCTNCCNAAATTNCNNANTTCCNCNTTCCNNCNTTT
CGGNTNNTCCCATNCTTTCCANNCTTCANTCTANCNCNCTNCAACTTATTTTCTTNCATCCCTTNTTCTTTACA
NNCCCCCTNNTCTACTCNCNNTTNCATTANATTTGAACTNCCACNNCTANTTNCCTCNCTCTACNNTTTTATTT
TNCGNTCNCTCTACNTAATANTTTAATNANTTNTCN

12_16474.edit

TCGAGCGGCCGCCCCGGGCAGGTCTGCCAAGGAGACCCTGTTATGCTGTGGGGACTGGCTGGGGCATGGCAGGCGGC
TCTGGCTTCCCACCCTTCTGTTCTGAGATGGGGGTGGTGGGCAGTATCTCATCTTTGGGTTCCACAATGCTCACGT
GGTCAGGCAGGGGCTTCTTAGGGCCAATCTTACCAGTTGGGTCCCAGGGCAGCATGATCTTCACCTTGATGCCAG
CACACCCTGTCTGAGCAACACGTGGCGCACAAGCAGTGTCAACGTAGTAAGTTAACAGGGTCTCCGCTGTGGATCA
TCAGGCCATCCACAACTTCATGGATTTAGCCCTCTGTCTCGGAGTTTCCAGACACCACAACCTCGCAGCCTTT
GGCCCCACTCTCCATGATGAACCGCAGCACACCATAGCAGGCCCTCCGCACAAGCAAGCCCTCCTAAGAATTTGTA
ACGCANANACTCTGCTGGCAATGGCACACAAACCTCTAGTGGACCTCGGNCGCGACCACGC

13_16475.edit

TCGAGCGGCCGCCCCGGGCAGGTCTGGTCCAGGATAGCCTGCGAGTCCTCCTACTGCTACTCCAGACTTGACATCAT
ATGAATCATACTGGGGAGAATAGTTCTGAGGACCAGTAGGGCATGATTCACAGATTCAGGGGGGCCAGGAGAACC
AGGGGACCCTGGTTGTCTGGAATACCAGGGTCACCATTTCTCCAGGAATACCAGGAGGGCCTGGATCTCCCTTG
GGGCCTTGAGGTCTTGACCATTAGGAGGGCGAGTAGGAGCAGTTGGAGGCTGTGGGCAAACTGCACAACATTCTC
CAAATGGAATTTCTGGGTTGGGGCAGTCTAATTCTTGATCCGTACATATTATGTATCGCAGAGAACGGATCCTG
AGTCACAGACACATATTTGGCATGGTTCTGGCTTCCAGACATCTCTATCCGNCATAGGACTGACCAAGATGGGAAC
ATCCTCCTTCAACAAGCTTNCTGTTGTGCCAAAAATAATAGTGGGATGAAGCAGACCGAGAAGTANCCAGCTCCCC
TTTTTGCACAAAGCNTCATCATGTCTAAATATCAGACATGAGACTTCTTTGGGCAAAAAGGAGAAAAAGAAAAAG
CAGTTCAAAGTANCCNCCATCAAGTTGGTTCCTTGCCNTTCAGCACCCGGGCCCCGTTATAAAACACCTNGGGCC
GGACCCCCCTT

14_16475.edit

AGCGTGGTCGCGGCCGAGGTGTTTTATGACGGGCGCGGTGCTGAAGGGCAGGGAACAACCTTGATGGTGCTACTTTG
AACTGCTTTTCTTTTCTCCTTTTGCACAAAGAGTCTCATGTCTGATATTTAGACATGATGAGCTTTGTGCAAAAG
GGGAGCTGGCTACTTCTCGCTCTGCTTATCCCACTATTATTTGGCACAACAGGAAGCTGTTGAAGGAGGATGTT
CCCATCTTGGTCAGTCTATGCGGATAGAGATGTCTGGAAGCCAGAACCATGCCAAATATGTGTCTGTGACTCAGG
ATCCGTTCTCTGCGATGACATAATATGTGACGATCAAGAATTAGACTGCCCCAACCCAGAAATTCATTTGGAGAA
TGTGTGTCAGTTTGGCCACAGCCTCCAACCTGCTCCTACTCGCCCTCCTAATGGTCAAGGACCTCAAGGCCCCAAGG
GAGATCCAGGCCCTCCTGGTATTCCTGGGAGAAATGGTGACCCTGGTATTCAGGACAACCAGGGTCCCCTGGTTC
TCCTGGCCCCCTGGAATCNGGNGAATCATGCCCTACTGGTCTCAAACCTATTCTCCANATGATTGATATGATGT
CAAGTCTGGGATAGCNAGTANGGANGGACTCGCAGGCTATTCTGGACCANACCTGCCGGGGGGGCGTTTCGAAAGCC
CGAATCTGCANANNTNCNTTCACACTGGCGGCCGTCGAGCTGCTTTAAAAGGGCCATTCCNCCTTTAGNGNGGGGG
ANTACAATTACTNGGCGGCGTTTTANANCGCGNGNCTGGGAAAT

15_16476.edit

AGCGTGGTCGCGGCCGAGGTCCACATCGGCAGGGTCGGAGCCCTGGCCGCCATACTCGAACTGGAATCCATCGGTC
ATGCTCTCGCCGAACCAGACATGCCTCTTGTCTTGGGGTCTTGCTGATGTACCAGTTCTTCTGGGCCACACTGG
GCTGAGTGGGGTACACGCAGGTCTCACCAGTCTCCATGTTGCAGAAGACTTTGATGGCATCCAGGTTGCAGCCTTG
GTTGGGGTCAATCCAGTACTCTCCACTCTTCCAGTCAGAGTGGCACATCTTGAGGTACGGCAGGTGCGGGCGGGG
TTCTTGGCGCTGCCCTCTGGGCTCCGGATGTTCTCGATCTGCTGGCTCAGGCTCTTGAGGGTGGTGTCCACCTCGA
GGTCACGGTCACGAACCACATTGGCATCATCAGCCCGGTAGTAGCGGCCACCATCGTGAGCCTTCTCTTGANGTGG
CTGGGGCAGGAACTGAAGTCGAAACCAGCGCTGGGAGGACCAGGGGGACCAANAGGTCCAGGAAGGGCCCGGGGG
GACCAACAGGACCAGCATCACCAAGTGCGACCCGCGAGAACCTGCCCGGCCGNCCTCGAA

16_16476.edit

TCGAGCGNNGCCCCGGGCAGGTCTCGCGGTGCACTGGTGATGCTGGTCCTGTTGGTCCCCCGGCCCTCCTGGAC
CTCCTGGTCCCCCTGGTCCTCCCAGCGCTGGTTTCGACTTCAGCTTCTGCCCCAGCCACCTCAAGAGAAGGCTCA
CGATGGTGGCCGCTACTACCGGGCTGATGATGCCAATGTGGTTCGTGACCGTGACCTCGAGGTGGACACCACCTC
AAGAGCCTGAGCCAGCAGATCGAGAACATCCGGAGCCCAGAGGGCAGCCGCAAGAACCCCCGCCGCACCTGCCGTG
ACCTCAAGATGTGCCACTCTGACTGGAAGAGTGGAGAGTACTGGATTGACCCCAACCAAGGCTGCAACCTGGATGC
CATCAAAGTCTTCTGCAACATGGAGACTGGTGAGACCTGCGTGTACCCCACTCAGCCAGTGTGGCCAGAAGAAC
TGGTACATCAGCAAGAACCCCAAGGACAAGAGGCATGTCTGGTTCGGCGAGAGCATGACCGATGGATTCCAGTTTCG
AGTATGGCGGCCAGGGCTCCCACCCTGCCGATGTGGACCTCCGGCCGCGACCACCTT

Fig. 15HH

17_16477.edit

TNGAGCGGCCGCCCCGGGCAGGNTGNNAACGCTGGTCCTGCTGGTCCTCCTGGCAAGGCTGGTGAAGATGGTCACCC
TGGAAAACCCGGACGACCTGGTGAGAGAGGAGTTGTTGGACCACAGGGTGCTCGTGGTTTTCCCTGGAACCTCCTGGA
CTTCCTGGCTTCAAAGGCATTAGGGGACACAATGGTCTGGATGGATTGAAGGGACAGCCCGGTGCTCCTGGTGTGA
AGGGTGAACCTGGTGCCCTGGTGAATGGAACCTCAGGTCAAACAGGAGCCCGTGGGCTTCCTGGTGAGAGAGG
ACCGTGTGGTGCCCTGGCCCANACCTCGGCCGCGACCACGCTAAGCCCGAATTTCCAGCACACTGGNGGCCGTT
ACTANTGGATCCGAGCTCGGTACCAAGCTTGGCGTAATCATGGTCATAGCTGTTTCCTGNGTGAAATTGTTATCCG
CTCACAATTTACACANCATACGAAGCCGGAAGCATAAAGTGTAAGCCTTGGGGTGCTAATGAGTGAGCTAACT
CNCATTAAATTGCGTTGCGCTCACTGCCCCGCTTTCCANNNGGGAACCNCTGGCNTNGCCNGCTTGCNTTAANTGA
AATCCGCCNACCCCGGGGAAAAGNCGGTTTGCNGTATTGGGGCNCCTTTTCCCTTTCCTCGGNTTACTTGANTTA
NTGGGCTTTGGNCGNTTCGGGTTGNGGCGANCNGTTCAACNTCACNCCAAAGGNGGNAANACGGTTTTCCCANAA
TCCGGGGGNTANCCCAANGNAAAACATNNGNCNAANGGGCT

18_16477.edit

AGCGTGGTTNGCGGCCGAGGTCTGGGCCAGGGGCACCAACACGTCCTCTCTCACCAGGAAGCCACGGGCTCCTGT
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CCATNCAGACCATTTGTGNCCCCTAATGCCCTTGAAGCCAGGAAGTCCAGGAGTTCCAGGGAAACCACCGAGCACCC
TGTGGTCCAACAACCTCTCTCACCAGGTCTCGGGTTTTCCAGGGTGACCATCTTACCAGCCTTGCCAGGAG
GACCAGCAGGACCAGCGTTACCAACCTGCCCCGGGCGGCCGCTCGA

21_16479.edit

TCGAGCGGCCGCCCCGGGCAGGTCCATTTTCTCCCTGACGGTCCCACTTCTCTCCAATCTTGTAGTTCACACCATTG
TCATGGCACCATCTAGATGAATCACATCTGAAATGACCACTTCCAAAGCCTAAGCACTGGCACAACAGTTTAAAGC
CTGATTGAGACATTGTTCCCACTCATCTCCAACGGCATAATGGGAACTGTGTAGGGGTCAAAGCACGAGTCATC
CGTAGGTTGGTTCAAGCCTTCTGTGACAGAGTTGCCACGGTAACAACCTCTTCCCGAACCTTATGCCTCTGCTGG
TCTTTCAGTGCCTCCACTATGATGTTGTAGGTGGCACCTCTGGTGAGGACCTCGGCCGCGACCACGCT

22_16479.edit

AGCGTGGTCGCGGCCGAGGTCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCAGCAGA
GGCATAAGGTTCCGGGAAGAGGTGTTACCGTGGGCAACTCTGTCAACGAAGGCTTGAACCAACCTACGGATGACTC
GTGCTTTGACCCCTACACAGTTTCCATTATGCCGTTGGAGATGAGTGGGAACGAATGTCTGAATCAGGCTTTAA
CTGTTGTGCCAGTGCTTAGGCTTTGGAAGTGGTCATTTCAAGATGTGATTCATCTAGATGGTGCCATGACAATGGT
GTGAACATAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGACCTGCCCGGGCCGGCCGCTCGA

Fig. 15II

24_16480.edit

TCGAGCGNNCGCCCGGGCAGGTCCAGTAGTGCCTTCGGGACTGGGTTCACCCCCAGGTCTGCGGCAGTTGTCACAG
CGCCAGCCCCGCTGGCCTCCAAAGCATGTGCAGGAGCAAATGGCACCGAGATATTCCTTCTGCCACTGTTCTCCTA
CGTGGTATGTCTTCCCATCATCGTAACACGTTGCCTCATGAGGGTCACACTTGAATTCTCCTTTCCGTTCCCAAG
ACATGTGCAGCTCATTTGGCTGGCTCTATAGTTTGGGGAAAGTTTGTGAAACTGTGCCACTGACCTTTACTTCCT
CCTTCTCTACTGGAGCTTTTCGTACCTTCCACTTCTGCTGTTGGTAAAATGGTGGATCTTCTATCAATTTATTGAC
AGTACCCACTTCTCCCAAACATCCAGGGAAATAGTGATTTAGAGCGATTAGGAGAACCAAATTATGGGGCAGAAA
TAAGGGGCTTTTCCACAGGTTTTCCTTTGGAGGAAGATTTAGTGGTGACTTTAAAAGAATACTCAACAGTGTCTT
CATCCCCATAGCAAAGAAGAAACNGTAAATGATGGAANGCTTCTGGAGATGCCNNCATTTAAGGGACNCCCAGAA
CTTACCATCTACAGGACCTACTTCAGTTTACANNAAGNCACATANTCTGACTCANAAAGGACCCAAGTAGCNCCA
TGGNCAGCACTTTNAGCCTTTCCCTGGGGAAAANNTTACNTTCTTAAANCCTNGGCCNNGACCCCTTAAGNCCA
AATTNTGGAAAANTTCNTNCCNCTGGGGGGCNGTTCNACATGCNTTNAAGGGCCCAATTNCCCCNT

25_16481.edit

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ATCTCCTCCCGGGATGGGGCAGGGTGTACACCTGTGGTTCTCGGGGCTGCCCTTTGGCTTTGGAGATGGTTTTCT
CGATGGGGGCTGGGAGGGCTTTGTTGGAGACCTTGCACCTGTACTCCTTGCCATTAGCCAGTCCTGGTGCAGGAC
GGTGAGGACGCTGACCACACGGTACGTGCTGTTGTACTGCTCCTCCCGCGGCTTTGTCTTGGCATTATGCACCTCC
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ACCTCGGCCGCGACACGCT

26_16481.edit

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AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACC
GTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAA
AGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAAGCCCCGAGAACCACAGGTGTACACCT
GCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTGACCTGACCTGCCTGGTCAAAGGCTTCTATCCAGCGAC
ATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACA
CCTGCCCCGGGCGGCCGCTCGA

27_16482.edit

TCGAGCGGCCCGCCCGGGCAGGTTGAATGGCTCCTCGCTGACCACCCCGGTGCTGGTGGTGGGTACAGAGCTCCGAT
GGGTGAAACCATTGACATAGAGACTGTCCCTGTCCAGGGTGTAGGGGCCAGCTCAGTGATGCCGTGGGTGAGCTG
GCTCAGCTTCCAGTACAGCCGCTCTCTGTCCAGTCCAGGGCTTTTGGGGTCAGGACGATGGGTGCAGACAGCATCC
ACTCTGGTGGCTGCCCCATCCTTCTCAGGCCTGAGCAAGGTGAGTCTGCAACCAGAGTACAGAGAGCTGACACTGG
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28_16482.edit

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CGTCCTGACCCCAAAGCCCTGGACTGGACAGAGAGCGGCTGTACTGGAAGCTGAGCCAGCTGACCCACGGCATCA
CTGAGCTGGGCCCCCTACACCCTGGACAGGGACAGTCTCTATGTCAATGGTTTCACCCATCGGAGCTCTGTACCCAC
CACCAGCACCGGGGTGGTCAGCGAGGAGCCATTCAACCTGCCCGGGCGGCCGCTCGA

29_16483.edit

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GTAGCCTCTGTGACACCAGGGCGGGGCCGAGGGACCCTTCTNTTGAAGAGACCAGCTTCTCATACTTGATGATGA
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ACTTTT

31_16484.edit

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GGACTCGTTTGTACCCGTTGATGATAGAATGGGGTACTGATGCAACAGTTGGGTAGCCAATCTGCAGACAGACT
GGCAACATTGCGGACACCCTCCAGGAAGCGAGAATGCAGAGTTTCTCTGTGATATCAAGCACTTCAGGGTTGTAG
ATGCTGCCATTGTGGAACACCTGCTGGATGACCAGCCCAAAGGAGAAGGGGGAGATGTTGAGCATGTTGAGCAGCG
TGGCTTCGCTGGCTCCCACTTTGTCTCCAGTCTTGATCAGACCTCGGCCGCGACCACGT

37_16487.edit

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AGCCCAAATCTTGACAAAACCTCACACATGCCACCGTGCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTT
CCTCTTCCCCCGCATCCCCCTTCCAAACCTGCCCGGGCGGCCGCTCG

38_16487.edit

CGAGCGGCCGCCCGGGCAGGTTTGGAAAGGGGGATGCGGGGGAAGAGGAAGACTGACGGTCCCCCAGGAGTTCAGG
TGCTGGGCACGGTGGGCATGTGTGAGTTTTGTCAAGATTTGGGCTCAACTCTCTTGTCCACCTTGGTGTTGCTG
GGCTTGATCTACGTTGCAGGTGTAGGTCTGGGTGCCGAAGTTGCTGGAGGGCAGGTCAACACGCTGCTGAGGG
AGTAGAGTCCTGAGGACTGTAGGACAGACCTCGGCCGCGACCACGT

39_16488.edit

NGGNNGGTCCGGNCNGNCAGGACCACTCNTCTTCGAAATA

41_16489.edit

AGCGTGGTCGCGGCCGAGGTCTCACTTGCCTCCTGCAAAGCACCGATAGCTGCGCTCTGGAAGCGCAGATCTGTT
TTAAAGTCCTGAGCAATTTCTCGCACCAGACGCTGGAAGGGAAGTTTGCGAATCAGAAGTTCAGTGGACTTCTGAT
AACGTCTAATTTACGGAGCGCCACAGTACCAGGACCTGCCCCGGGCGGCCGCTCGA

42_16489.edit

TCGAGCGGCCGCCCGGGCAGGTCTGGTACTGNGGCGCTCCGTGAAATTAGACGTTATCAGAAGTCCACTGAACTT
CTGATTCGCAAACTTCCCTTCCAGCGTCTGGTGCGAGAAATTGCTCAGGACTTTAAACAGATCTGCGCTTCCAGA
GCGCAGCTATCGGTGCTTTCAGGAGGCAAGTGAGGACCTCGGCCGCGACCACGT

45_16491.edit

TCGAGCGGCCGCCCGGGCAGGTCCACATCGGCAGGGTCGGAGCCCTGGCCGCCATACTCGAACTGGAATCCATCGG
TCATGCTCTCGCCGAACCAGACATGCCTCTTGTCTTGGGGTTCTTGCTGATGTACCAGTTCTTCTGGGCCACACT
GGGCTGAGTGGGGTACACGCAGGTCTCACCAGTCTCCATGTTGCAGAAGACTTTGATGGCATCCAGGTTGCAGCCT
TGGTTGGGGTCAATCCAGTACTCTCACTCTTCCAGTCAGAGTGGCACATCTTGAGGTACGGCAGGTGCGGGCGG
GGTTCTTGACCTCGGCCGCGACCACGT

46_16491.edit

GTGGGNTTGAACCCNTTTNANCTCCGCTTGGTACCGAGCTCGGATCCACTAGTAACGGCCGCCAGTGTGCTGGAAT
TCGGCTTAGCGTGGTCGCGGCCGAGGTCAAGAACCCGCCCCGACCTGCCGTGACCTCAAGATGTGCCACTCTGAC
TGGAAGAGTGGAGAGTACTGGATTGACCCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGG
AGACTGGTGAGACCTGCGTGTACCCCACTCAGCCCACTGTGGCCCAAGAAGTGGTACATCAGCAAGAACCCCAA
GGACAAGAGGGCATGTCTGGTTCGGCGAGAGCATGACCGATGGATTCCAGTTCGAGTATGGCGGCCAGGGCTCCGAC
CCTGCCGATGTGGACCTGCCCCGGCGGCCGCTCGA

47_16492.edit

AGCGTGGTCGCGGCCGAGGTCTGGGATGCTCCTGCTGTACAGTGAGATATTACAGGATCACTTACGGAGAAACAG
GAGGAAATAGCCCTGTCCAGGAGTTCAGTGTGCTGGGAGCAAGTCTACAGCTACCATCAGCGGCCTTAAACCTGG
AGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAGCCCCGCAAGCAGCAAGCCAATTTCCATT
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GGCTGCCTTCAAGTTCCTCTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAAC
TAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGACGCCACAGTGGAGTATGTGGTTAAGTGT
CTATGCTCAGAATCCAAGCGGAGAGAAGTCAGCCTCTGGTTCAGACTGNAAGTAACCAACATTGATCGCCTAAAGG
ACTGGCATTCACTGATGNGGATGCCGATTCCATCAAAATTGNTTGGGAAAACCCACAGGGGCAAGTTTNCANGTCN
AGGNGGACCTACTCGAGCCCTGAGGATGGAATCCTTGACTNTTCTTNNCCTGATGGGGAAAAAAAACCTTNAAAA
CTTGAAGGACCTGCCCCGGCGGCCGTNCAAAACCCAATTCCACCCCTTGGGGGCGTTCTATGGGNCCCACTCGGA
CCAAACTTGGGGTAAN

48_16492.edit

TCGAGCGGCCGCCCCGGGCAGGTCTTGCAGCTCTGCAGTGTCTTCTTACCATCAGGTGCAGGGAATAGCTCATGG
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TGGAATCGGCATCCACATCAGTGAATGCCAGTCTTTAGGGCGATCAATGTTGGTTACTGCAGTCTGAACCAGAGG
CTGACTCTCTCCGCTTGGATTCTGAGCATAGACACTAACCACATACTCCACTGTGGGCTGCAAGCCTTCAATAGTC
ATTTCTGTTTGATCTGGACCTGCAGTTTTAGTTTTTGTGGTCTGGTCCATTTTTGGGAGTGGTGGTTACTCTGT
AACCAGTAACAGGGGAACCTTGAAGGCAGCCACTTGACACTAATGCTGTTGTCCTGAACATCGGTCACTTGCATCTG
GGATGGTTTGTCAATTTCTGTTTCGGTAATTAATGGAAATTGGCTTGCTGCTTGCGGGGCTTGTCTCCACGGCCAGT
GACAGCATACACAGTGATGGTATAATCAACTCCAGGTTTAAAGCCGCTGATGGTAGCTGAAACTTTGCTCCAGGCAC
AAGTGAACCTCTGACAGGGCTATTTCTNCTGTTCTCCGTAAGTGATCCTGTAATATCTCACTGGGACAGCAGGAN
GCATTCCAAAACCTCGGGCGNGACCCCTAAGCCGAATTNTGCAATATNCATCACACTGGCGGGCGCTCGANCATT
CATTAAAAGGCCCAATCNCCTATAGGGAGTNTANTACAATTNG

Fig. 15MM

49_16493.edit

TCGAGCGGCCGCCCCGGGCAGGTCACTTTTGGTTTTTGGTCATGTTGCGTTGGTCAAAGATAAAAACTAAGTTTGAG
AGATGAATGCAAAGGAAAAAATATTTTCCAAAGTCCATGTGAAATTGTCTCCATTTTTTGGCTTTTGAGGGGG
TTCAGTTTGGGTTGCTTGTCTGTTTCCGGGTTGGGGGAAAGTTGGTTGGGTGGGAGGGAGCCAGGTTGGGATGGA
GGGAGTTTACAGGAAGCAGACAGGGCCAACGTCG

55_16496.edit

AGCGTGGTCGCGGCCGAGGTCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCAGCAGA
GGCATAAGGTTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTTGAACCAACCTACGGATGACTC
GTGCTTTGACCCCTACACAGTTTCCCATTATGCCGTTGGAGATGAGTGGGAACGAATGTCTGAATCAGGCTTTAA
CTGTTGTGCCAGTGCTTAGGCTTTGGAAGTGGTCATTTAGATGTGATTCATCTAGATGGTGCCATGACAATGGTG
TGAACATAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGACCTGCCCGGGCGGCCGCTCGA

56_16496.edit

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TCATGGCACCATCTAGATGAATCACATCTGAAATGAACACTTCCAAAGCCTAAGCACTGGCACAACAGTTTAAAGC
CTGATTCAGACATTCGTTCCCACTCATCTCCAACGGCATAATGGGAACTGTGTAGGGGTCAAAGCACGAGTCATC
CGTAGGTTGGTTCAAGCCTTCGTTGACAGAGTTGCCACGGTAACAACCTCTTCCCGAACCTTATGCCTCTGCTGG
TCTTTCAAGTGCCTCCACTATGATGTTGTAGGTGGCACCTCTGGTGAGGACCTCGGCCGCGACCACGCT

59_16498.edit

TCGAGCGGCCGCCCCGGGCAGGTCCACCATAAGTCCTGATACAACCACGGATGAGCTGTCAGGAGCAAGGTTGATTT
CTTTTATTGGTCCGGTCTTCTCCTTGGGGGTACCCGCACTCGATATCCAGTGAGCTGAACATTGGGTGGTGTCCA
CTGGGCGCTCAGGCTTGTGGGTGTGACCTGAGTGAACCTCAGGTGAGTTGGTGCAGGAATAGTGGTTACTGCAGTC
TGAACCAGAGGCTGACTCTCTCCGCTTGATTCTGAGCATAGACACTAACCACATACTCCACTGTGGGCTGCAAGC
CTTCAATAGTCATTTCTGTTTGATCTGGACCTGCAGTTTTAGTTTTTGTGGTCTGGTCCATTTTTGGGAGTGGT
GGTTACTCTGTAACCAGTAACAGGGGAACCTGAAGGCAGCCACTTGACACTAATGCTGTTGTCTGAACATCGGTC
ACTTGATCTGGGATGGTTTGNCAATTTCTGTTCCGTAATTAATGGAAATTGGCTTGCTGCTTGCGGGGCTGTCTC
CACGGCCAGTGACAGCATACAGNGATGGNATNATCAACTCCAAGTTTAAGGCCCTGATGGTAACTTTAAACTTG
CTCCAGCCAGNGAATTCGGACAGGGTATTTCTTCTGGTTTTCCGAAAGNGANCCTGGAATNNTCTCCTTGGAN
CAGAAGGANCTCCAAAACCTTGGGCCGGAACCCCTT

Fig. 15NN

60_16473.edit

AGCGTGGTCGCGGCCGAGGTCCTGTCAGAGTGGCACTGGTAGAAGTTCCAGGAACCCTGAACTGTAAGGGTTCTTC
ATCAGTGCCAACAGGATGACATGAAATGATGTACTCAGAAGTGCTCGGAATGGGGCCCATGAGATGGTTGTCTGA
GAGAGAGCTTCTTGCTCTACATTGCGCGGGTATGGTCTTGGCCTATGCCTTATGGGGGTGGCCGTTGTGGGCGGTG
TGGTCCGCCTAAAACCATGTTCTCAAAGATCATTTGTTGCCAACACTGGGTTGCTGACCAGAAGTGCCAGGAAG
CTGAATACCATTTCCAGTGTACATCCAGGGTGGGTGACGAAAGGGGTCTTTGAACTGTGGAAGGAACATCCAAG
ATCTCTGGTCCATGAAGATTGGGGTGTGGAAGGGTTACCAGTTGGGGAAGCTCGTCTGTCTTTTTCTTCCAATCA
GGGGCTCGCTCTTCTGATTATTCTTCAGGGCAATGACATAAATTGTATATTCGGTTCCTGGTTCAGGCCAGTAAT
AGTAGCCTCTTGTGACACCAGGCGGGGCCANGGACCACTTCTCTGGGANGAGACCCAGCTTCTCATACTTGATGA
TGTAACCCGGTAATCCTGCACGTGGCGGCTGNCATGATACCANCAAGGAATTGGGTGNGGNGGACCTGCCCGGCGG
CCCTCNA

60_16498.edit

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AGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAGCCCCGCAAGCAGCAAGCCAATTTCCATT
AATTACCGAACAGAAATTGACAAACCATCCAGATGCAAGTGACCGATGTTTACAGGACAACAGCATTAGTGTCAAGT
GGCTGCCTTCAAGTTCCCTGTACTGGTTACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAAC
TAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGACAGCCACAGTGGAGTATGTGGTTAGTGTC
TATGCTCAGAATCCAAGCGGAGAGAGTCAAGCTCTGGTTCAGACTGCAGTAACCACTATTCTGCACCAACTGACC
TGAAGTTCACTCAGGTACACCCACAAGCCTGAGCCGCCAGTGGACACCACCAATGTTCACTCACTGGATATCGA
GTGCGGGTGACCCCAAGGAGAAGACCCGGACCCATGAAAGAAATCAACCTTGCTCCTGACAGCTCATCCGNGGGT
GTATCAGGACTTATGGGGGACTGCCCGGCGNGCCGNTCGAAANCGAATTNTGAAATTTCTTCNCACTGGGNGGC
GNTTCGAGCTTNTTNTANANGGCCCAATTCNCCTNTAGNGGGTCTGN

61_16499.edit

AGCGTGGTCGCGGCCGAGGTCNAGG

62_16483.edit

TCGAGCGGCCGCGCCGGGCAGGTCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACGTGCCAGGATTA
CCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCAGAGAAGTGGTCCCTCGGCCCGCCCTGGTGTAC
AGAGGCTACTATTACTGGCCTGGAACCGGGAACCGAATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAG
AGCGAGCCCTGATTGGAAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCTTCCACACCCCAATCTTCATG
GACCAGAGATCTTGATGTTCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCACCCTGGGTATGACACTGGAAA
TGGTATTCACTTCTTGGCACTTCTGGTCAGCAACCCAGTGTGGGCAACAAATGATCTTTGAGGAACATGGTTTT
AGGCGGACCACACCGCCCAACGGGCACCCCATAGGNAAGGCAAGACCATACCCCGCCGAATGTAGGACAA
GAAGCTCTNTCTCAACAACCATCTCATGGGCCCCATTCCAGGACACTTCTGAGTACATCATTTTCATGTCATCTGG
TGGGCACTTGATGAANAACCTTACAGTTCAAGGTTCTGGAACCTTCTACCAGNGCCACTTCTGACAGGANCTTGG
GCGNGACCAACCT

63_16500.edit

AGCGTGGTCGCGGCCGAGGTCCATTTTCTCCCTGACGGTCCCACTTCTCTCCAATCTTGTAGTTCACACCATTGTC
ATGGCACCATCTAGATGAATCACATCTGAAATGACCACTTCCAAAGCCTAAGCACTGGCACAACAGTTTAAAGCCT
GATTCAGACATTGTTCCCACTCATCTCCAACGGCATAATGGGAACTGTGTAGGGGTCAAAGCACGAGTCATCCG
TAGGTTGGTTCAAGCCTTCGTTGACAGAGTTGCCACGGTAACAACCTCTTCCCGAACCTTATGCCTCTGCTGGTC
TTTCAGTGCCTCCACTATGATGTTGTAGGTGGCACCTCTGGTGAGGACCTGCCCGGGCGGCCCGCTCGA

64_16493.edit

AGCGTGGTCGCGGCCGAGGTGTGCCCCAGACCAGGAATTCGGCTTCGACGTTGGCCCTGTCTGCTTCCTGTAACT
CCCTCCATCCCAACCTGGCTCCCTCCCACCCAACCAACTTTCCCCCAACCCGGAACAGACAAGCAACCCAACT
GAACCCCTCAAAGCCAAAAAATGGGAGACAATTTACATGGACTTTGGAAAATATTTTTTCTTTGCATTCA
TCTCTCAAACCTAGTTTTTATCTTTGACCAACCGAACATGACCAAAAACCAAAAGTGACCTGCCCGGGCGGCCGCT
CGA

64_16500.edit

TCGAGCGGCCGCCCCGGGCAGGTCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCAGCA
GAGGCATAAGGTTGCGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTTGAACCAACCTACGGATGAC
TCGTGCTTTGACCCCTACACAGTTTCCCATTTATGCCGTTGGAGATGAGTGGGAACGAATGTCTGAATCAGGCTTTA
AACTGTTGTGCCAGTGCTTAGGCTTTGGAAGTGGTCATTTTCAATGTGATTATCTAGATGGTGCCATGACAATGG
TGTGAACTACAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGACCTCGGCCGCGACCACGCT

Fig. 15PP

16501.edit

TCGAGCGGCCGCCCCGGGCAGGTACCGGGGTGGTCAGCGAGGAGCCATTCACTGAACCTTCACCATCAACAACCTG
CGGTATGAGGAGAACATGCAGCACCCCTGGCTCCAGGAAGTTCAACACCACGGAGAGGGTCTTCAGGGCCTGCTCA
GGTCCCTGTTCAAGAGCACCAAGTGTGGCCCTCTGTACTCTGGCTGCAGACTGACTTTGCTCAGACCTGAGAAACA
TGGGGCAGCCACTGGAGTGGACGCCATCTGCACCCTCCGCCTTGATCCCACTGGTNTCTGGACTGGACANANAGCGG
CTATACTTGGGAGCTGANCCNAACCTTTGGCGGNGACNCCNCTT

16501.2.edit

GAGGACTGGCTCAGCTCCCAGTATAGCCGCTCTCTGTCCAGTCCAGGACCAGTGGGATCAAGGCGGAGGGTGCAGA
TGGCGTCCACTCCAGTGGCTGCCCCATGTTTCTCAAGTCTGAGCAAAGNCAGTCTGCAGCCAGAGTACAGAGGGCC
AACACTGGTGCTCTTGAACAGGGACCTGAGCAGGCCCTGAAGGACCCTCTCCGTGGTGTGAACTTCTGGAGCCA
GGGTGCTGCATGTTCTCCTCATACCGCAGGTTGTTGATGGTGAAGTTCAGTGTGAATGGCTCCTCGCTGACCACCC

16502.1.edit

AGCGTGGTCGCGGCCGAGGTCCACCACACCCAATTCTTGCTGGTATCATGGCAGCCGCCACGTGCCAGGATTACC
GGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGTGGTCCCTCGGCCCCGCCCTGGTGTACAG
AGGCTACTATTACTGGCCTGGAACCGGGAACCGAATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAGAG
CGAGCCCCCTGATTGGAAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGGA
CCANANANCTTGGATNGTCCTTTCACNGGTTNAAAAAACCTTTTCGCCCCCCCACCTTGGGGATTAACCTTGGGA
AANGGGGATTTNACCNTTCC

16502.2.edit

TCGAGCGGCCGCCCCGGGCAGGTCTGTGAGAGTGGCACTGGTAGAAGTTCAGGAACCCTGAACTGTAAGGGTTCT
TCATCAGTGCCAACAGGATGACATGAAATGATGTACTCAGAAGTGTCTGGAATGGGGCCCATGAGATGGTTGTCT
GAGAGAGAGCTTCTTGTCTACATTCGGCGGGTATGGTCTTGGCCTATGCCTTATGGGGGTGGCCGTTGTGGGCGG
TGTGGTCCGCCTAAAACCATGTTCTCAAAGATCATTTGTTGCCAACACTGGGTTGCTGACCAGAAGTGCCAGGA
AGCTGAATAACCATTTCCAGTGTATACCCAGGGNGGGTGACCAAGGGGGTCNTTTNGACCTGGNGAAAGGAACCA
TCCAAAANCTCTGNCCCATG

Fig. 15QQ

16503.1.edit

AGCGTGGNCGCGGCCGAGGTCTGAGGATGTAACTCTTCCCAGGGGAAGGCTGAAGTGCTGACCATGGTGCTACTG
GGTCCTTCTGAGTCAGATATGTGACTGATGNGAACTGAAGTAGGTACTGTAGATGGTGAAGTCTGGGTGTCCCTAA
ATGCTGCATCTCCAGAGCCTTCCATCATTACCGTTTCTTCTTTTGCTATGGGATGAGACACTGTTGAGTATTCTCT
AAAGTCACCACTGAAATCTTCTCCAAAGGAAAACCTGTGGAAGGCCCCTTATTTCTGCCCCATAATTTGGTTCT
CCTAATCNCTCTGAAATCACTATTTCCCTGGAANGTTTGGGAAAAANNGGGCNACCTGNCANTGGAAANTGGATAN
AAAGATCCCACCATTTTACCCAACNAGCAGAAAGTGGGAANGGTACCGAAAAGCTCCAAGTAANAAAAAGGAGGGA
AGTAAAGGTCAAGTGGGCACCAGTTTCAAACAAAACCTTTCCCAAACCTATANAACCCA

16503.2.edit

AAGCGGCCGCCCCGGGCAGGNNCAGNAGTGCCTTCGGGACTGGGNTCACCCCCAGGTCTGCGGCAGTTGTACAGCG
CCAGCCCCGCTGGCCTCCAAAGCATGTGCAGGAGCAAATGGCACCGAGATATTCCTTCTGCCACTGTTCTCCTACG
TGGTATGTCTTCCCATCATCGTAACACGTTGCCTCATGAGGGTCACACTTGAATTCTCCTTTTCCGTTCCCAAGAC
ATGTGCAGCTCATTTGGCTGGCTCTATAGTTTGGGAAAGTTTGTGAACTGTGCCACTGACCTTTACTTCCTCC
TTCTCTACTGGAGCTTTCCGTACCTTCCACTTCTGCTGNTGGNAAAAAGGGNGGAACNTCTTATCAATTTCAATTGG
ACAGTANCCCNCTTTCTNCCCAAACATNCAAGGGAAAATATTGATTNCNAGAGCGGATTAAGGAACAACCCNAAT
TATGGGGGCCAGAAATAAAGGGGGCTTTTCCACAGGTNTTTTCT

16504.1.edit

TCGAGCGGCCGCCCCGGGCAGGTCTGCAGGCTATTGTAAGTGTTCTGAGCACATATGAGATAACCTGGGCCAAGCTA
TGATGTTTCGATACGTTAGGTGTATTAAATGCACTTTTGACTGCCATCTCAGTGGATGACAGCCTTCTCACTGACAG
CAGAGATCTTCCTCACTGTGCCAGTGGGCAGGAGAAAGAGCATGCTGCGACTGGACCTCGGCCGCGACCACGCT

16504.2.edit

AGCGTGGTCGCGGCCGAGGTCCAGTCGCAGCATGCTCTTTCTCCTGCCCACTGGCACAGTGAGGAAGATCTCTGCT
GTCAGTGAGAAGGCTGTCATCCACTGAGATGGCAGTCAAAGTGCATTTAATACACCTAACGTATCGAACATCATA
GCTTGGCCAGGTTATCTCATATGTGCTCAGAACACTTACAATAGCCTGCAGACCTGCCCGGGCGGCCGCTCGA

16505.1.edit

CGAGCGGCCGCCCCGGGCAGGTCCAGACTCCAATCCAGAGAACCACCAAGCCAGATGTCAGAAGCTACACCATCACA
GGTTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAATGACAAATGCTCGGAGCTCCCCTGTGGTCA
TCGACGCCTCCACTGCCATTGATGCACCATCCAACCTGCGTTTCCTGGCCACCACACCCAATTCCTTGCTGGTATC
ATGGCAGCCGCCACGTGCCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGTG
GTCCCTCGGCCCGCCCTGGTGNCACAGAAGCTACTATTACTGGCCTGGAACCGGAACCGAATATACAATTTATG
TCATTGCCCTGAAGAATAATCANAAGAGCGAGCCCTGATTGGAAGG

16505.2.edit

AGCGTGGTCGCGGCCGAGGTCTGTGAGAGTGGCACTGGTAGAAGTTCCAGGAACCCTGAACTGTAAGGGTTCTTC
ATCAGTGCCAACAGGATGACATGAAATGATGTACTCAGAAGTGTCTGGAATGGGGCCCATGAGATGGTTGTCTGA
GAGAGAGCTTCTTGCTCTGTCTTTTTCTTCCAATCAGGGGCTCGCTCTTCTGATTATTCTTCAGGGCAATGACAT
AAATTGTATATTCGGTTCCTGGTTCAGGCCAGTAATAGTAGCCTCTGTGACACCAGGGCGGGGCCGAGGGACCAC
TTCTCTGGGAGGAGACCCAGGCTTCTCATACTTGATGATGTANCCGGTAATCCTGGCACCGTGGCGGCTGCCATGA
TACCAGCAAGGAATTGGGTGTGGTGGCCAAGAAACGCAGGTTGGATGGTGCATCAATGGCAGTGGAGGCGTTCGATN
ACCACAGGGGAGCTCCGANCATTGTCATTCAAGGTGGACAGGTAGAATCTTGTAATCAGGTGCCTGGTTTGTAAC
CTG

16506.1.edit

TCGAGCGGCCGCCCCGGGCAGGTTTCGTGACCGTGACCTCGAGGTGGACACCACCCTCAAGAGCCTGAGCCAGCAGA
TCGAGAACATCCGGAGCCCAGAGGGCAGCCGCAAGAACCCCGCCGACCTGCCGTGACCTCAAGATGTGCCACTC
TGACTGGAAGAGTGGAGAGTACTGGATTGACCCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAAC
ATGGAGACTGGTGAGACCTGCGTGTACCCCACTCAGCCAGTGTGGCCCAGAAGAACTGGTACATCAGCAAGAACC
CCAAGGACAAGAAGCATGTCTGGTTCGGCGAAAGCATGACCGATGGATTCCAGTTCGAGTATGGCGGCCAGGGCTC
CGACCCTGCCGATGTGGACCTCGGCCGCGACCACGCTAAGCCCGAATTCCAGCACACTGGCGGCCGTTACTAGTGG
GATCCGAGCTTCGGTACCAAGCTTGGCGTAATCATGGGNCATAGCTGTTTCCTGNGTGAAAATGGTATTCCGCTTC
ACAATTTCCAC

16506.2.edit

AGCGTGGTCGCGGCCGAGGTCCACATCGGCAGGGTTCGAGGCCCTGGCCGCCATACTCGAACTGGAATCCATCGGTC
ATGCTCTCGCCGAACCAGACATGCCTCTTGCTCTTGGGGTCTTGCTGATGTACCAGTTCTTCTGGGCCACACTGG
GCTGAGTGGGGTACACGCAGGTCTCACCAGTCTCCATGTTGCAGAAGACTTTGATGGCATCCAGGTTGCAGCCTTG
GTTGGGGTCAATCCAGTACTCTCCACTCTTCCAGTCAGAGTGGCACATCTTGAGGTACGGCAGGTGCGGGCGGGG
TTCTTGCGGCTGCCCTCTGGGCTCCGGATGTTCTCGATCTGCTGGCTCAAGCTCTTGAAGGGTGGTGTCCACCTCG
AGGTCACGGTCACGAAACCTGCCCGGGCGGCCGCTCGA

16507.1.edit

AGCGTGGTCGCGGCCGAGGTCAAGAACCCCGCCCGCACCTGCCGTGACCTCAAGATGTGCCACTCTGACTGGAAGA
GTGGAGAGTACTGGATTGACCCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGGAGACTGG
TGAGACCTGCGTGTACCCCACTCAGCCCACTGTGGCCAGAAAGAACTGGTACATCAGCAAGAACCCCAAGGACAAG
AGGCATGTCTGGTTCCGCGAGAGCATGACCGATGGATTCCAGTTCGAGTATGGCGGCCAGGGCTCCGACCCTGCCG
ATGTGGACCTGCCCGNGCCGNCCTCGAAAAGCCNAATTTCCAGNCACACTTGGCCGGCCGTTACTACTG

16507.2.edit

TCGAGCGGCCGCCCCGGGCAGGTCCACATCGGCAGGGTCGGAGCCCTGGCCGCCATACTCGAACTGGAATCCATCGG
TCATGCTCTCGCCGAACCAGACATGCCTCTTGTCTTGGGGTCTTGTCTGATGTACCAGTTCTTCTGGGCCACACT
GGGCTGAGTGGGGTACACGCAGGTCTCACCAGTCTCCATGTTGCAGAAGACTTTGATGGCATCCAGGTTGCAGCCT
TGGTTGGGGTCAATCCAGTACTCTCCACTCTTCCAGTCAGAGTGGCACATCTTGAGGTACCGGCAGGTGCGGGCGG
GGTTCTTGACCTCGGCCGCGACCACGCT

16508.1.edit

CGAGCGGCCGCCCCGGGCAGGTCCCCCCCCTT
TTTTTTTTTTTTTTTTTT

16508.2.edit

AGCGTGGTCGCGGCCGAGGTCTGGCATTCTTCTGACTTCTCTCCAGCCGAGCTTCCCAGAACATCACATATCACTG
CAAAAATAGCATTGCATACATGGATCAGGCCAGTGGAAATGTAAAGAAGGCCCTGAAGCTGATGGGGTCAAATGAA
GGTGAATTCAAGGCTGAAGGAAATAGCAAATTCACCTACACAGTTCTGGAGGATGGTTGCACGAAACACACTGGGG
AATGGAGCAAAACAGTCTTTGAATATCGAACACGCAAGGCTGTGAGACTACCTATTGTAGATATTGCACCCTATGA
CATTGGTGGTCTGATCAAGAATTTGGTGTGGACGTTGGCCCTGTTTGTCTTTTATAAACCAAACTCTATCTGAAA
TCCCAACAAAAAAATTTAACTCCATATGTGNTCCTCTTGTCTAATCTTGGCAACCAGTGAAGTGACCGACAAA
ATTCCAGTTATTTATTTCCAAAATGTTTGGAAACAGTATAATTTGACAAAGAAAAAAGGATACTTCTTTTTTTTG
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TGGNGCTTATAATAAAATAAACTTTACCCTTNTTTNTGAT

16509.1.edit

AGCGTGGTCGCGGCCGAGGTCTGGGATGCTCCTGCTGTACAGTGAGATATTACAGGATCACTTACGGAGAAACAG
GAGGAAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGGCCTTAAACCTGG
AGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAGCCCCGCAAGCAGCAAGCCAATTTCCATT
AATTACCGAACAGAAATTGACAAACCATCCAGATGCAAGTGACCGATGTTCAAGGACAACAGCATTAGTGTCAAGT
GGCTGCCTTCAAGTTCCCCTGTTACTGGTTACAGAAAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAA
CTAAACTGCAGGTCCAGATCAAACAGAAAATGGACTATTGAAGGCTTGACGCCACAGTGGAAAGTATGTGGNTAG
NGTCTATGCTCAGAATCCCAAGCCGGAGAAAGTCAGCCTTCTGGTTTAGACTGCAGTAACCAACATTGATCGCCC
TAAAGGACTGGNCATTCACTTGGATGGTGGATGTCCAATTC

16509.2.edit

TCGAGCGGCCGCCCCGGGCAGGTCTTGCAGCTCTGCAGNGTCTTCTTCACCATCAGGTGCAGGGAATAGCTCATGG
ATTCCATCCTCAGGGCTCGAGTAGGTCAACCTGTACCTGGAACTTGCCCTGTGGGCTTTCCCAAGCAATTTTGA
TGAATCGACATCCACATCAGNGAATGCCAGTCTTTAGGGCGATCAATGTTGGTTACTGCAGTCTGAACCAGAGG
CTGACTCTCTCCGCTTGATTCTGAGCATAGACACTAACCACATACTCCACTGTGGGCTGCAAGCCTTCAATAGTC
ATTTCTGTTTGATCTGGACCTGCAGTTTTAAGTTTTTGGTGGTCTGNCCATTTTTGGGAAGTGGGGGGTACTC
TGTAACCAGTAACAGGGGAACCTGAAGGCAGCCACTTGACACTAATGCTGTTGTCTGAACATCGGTCACTTGCAT
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GGGCCAGTGACAGCATAC

16510.1.edit

TCGAGCGGCCGCCCCGGGCAGGTCTTGCAGCTCTGCAGTGTCTTCTTCACCATCAGGTGCAGGGAATAGCTCATGG
ATTCCATCCTCAGGGCTCGAGTAGGTCAACCTGTACCTGGAACTTGCCCTGTGGGCTTTCCCAAGCAATTTTGA
TGAATCGACATCCACATCAGTGAATGCCAGTCTTTAGGGCGATCAATGTTGGTTACTGCAGTCTGAACCAGAGG
CTGACTCTCTCCGCTTGATTCTGAGCATAGACACTAACCACATACTCCACTGTGGGCTGCAAGCCTTCAATAGTC
ATTTCTGTTTGATCTGGACCTGCAGTTTTAAGTTTTTGGTGGNCCTGNNCCATTTTTGGGGAAGGGGTGGTTACTC
TTGTAACCAGTAACAGGGGAACCTGAAGCAGCCACTTGACACTAATGCTGGTGGCCTGAACATCGGTCACTTGCAT
CTGGGATGGTTTGGTCAATTTCTGTTCCGTAATTAATGGGAAATTGGCTTACTGGCTTGCGGGGGCTGTCTCCAGG
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16510.2.edit

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16511.2.edit

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Fig. 15DDD

07_16537.1.edit

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08_16537.2.edit

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Fig. 15EEE

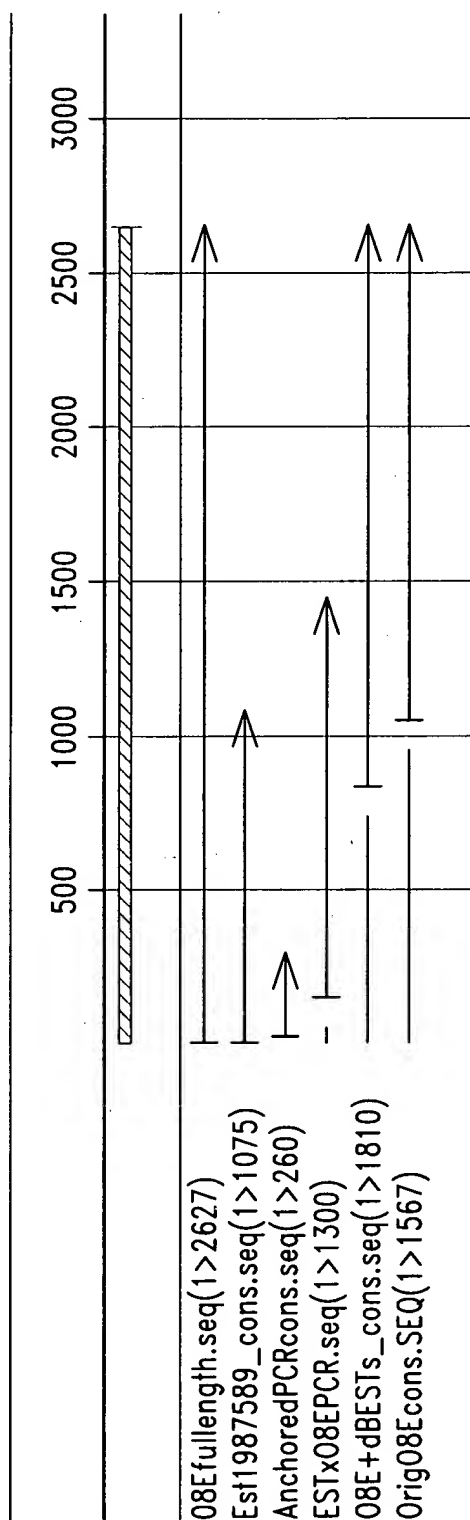


Fig. 16

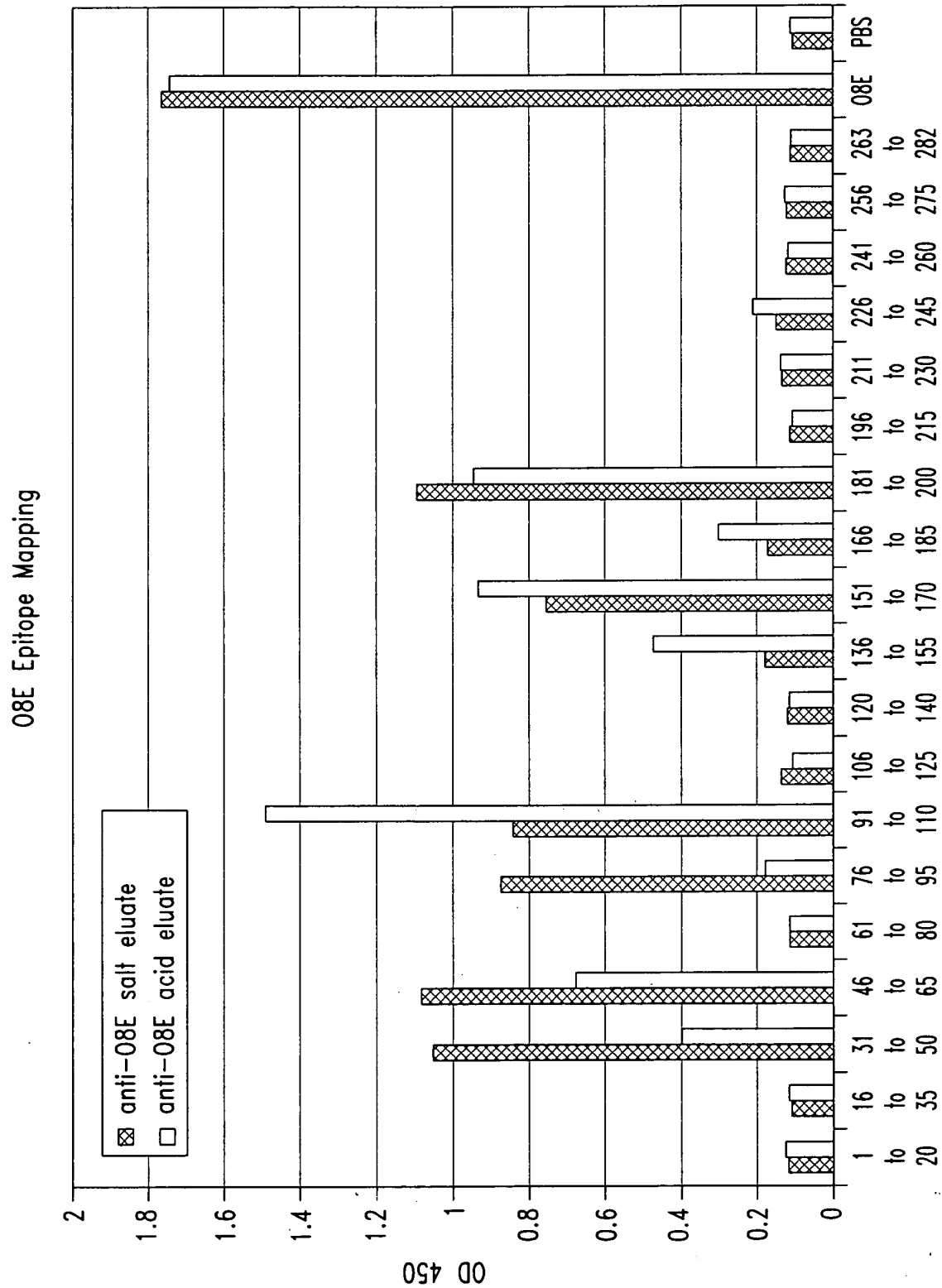
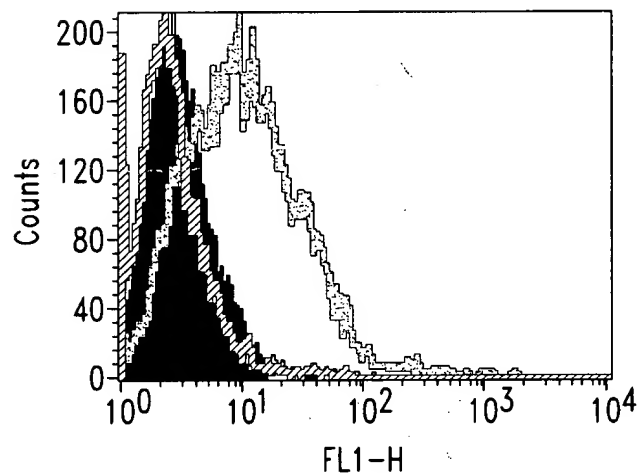


Fig. 17

O8E Surface Expression



- B305D/HEK stained with anti-O8E antibody
- O8E/HEK stained with anti-O8E antibody
- /// O8E/HEK stained with an irrelevant antibody

Fig. 18

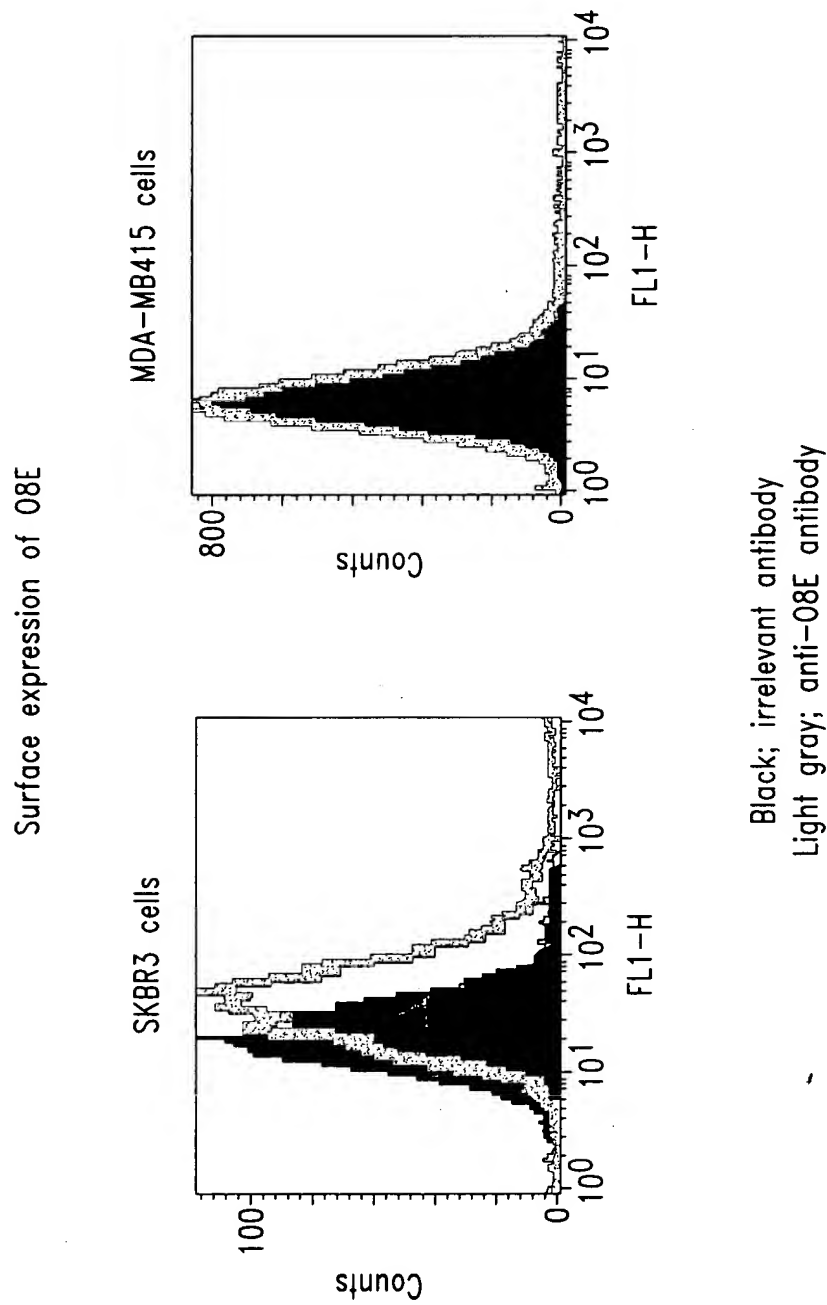
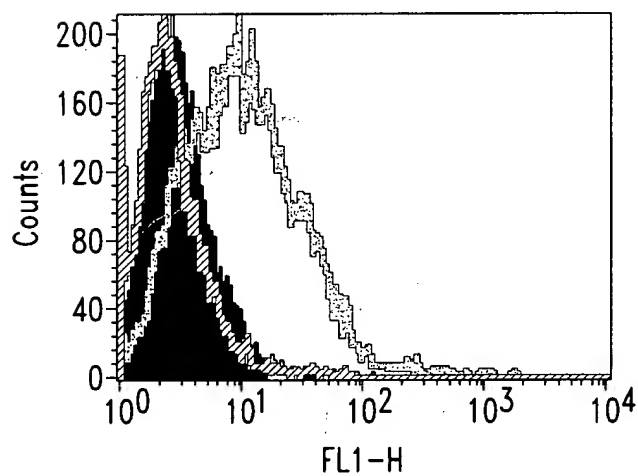


Fig. 19

O8E Surface Expression



- B305D/HEK stained with anti-O8E antibody
- O8E/HEK stained with anti-O8E antibody
- ▨ O8E/HEK stained with an irrelevant antibody

Fig. 20

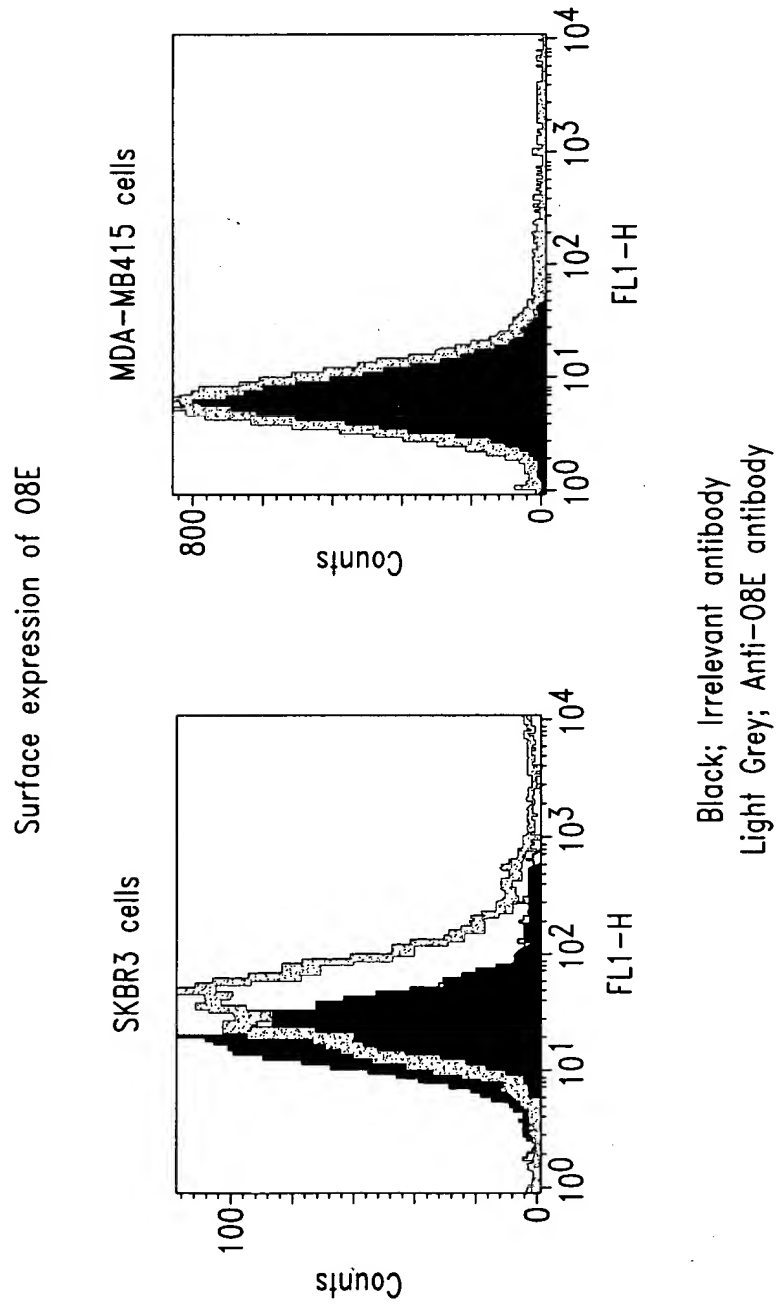


Fig. 21

O8E expression in HEK293 Cells
(probed with anti-O8E rabbit polyclonal sera #2333L)

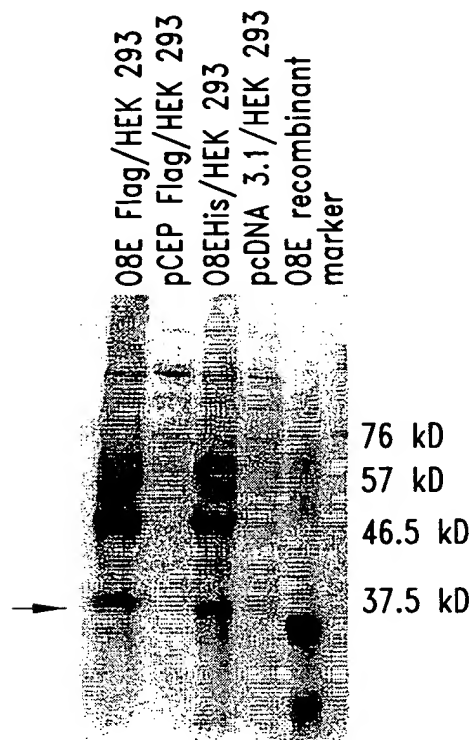


Fig. 22

08E Rabbits 01212000

Date: 1/21/99

| Antigen on Plate | Sera Sample | Antibody Dilutions | | | | | | | | | | | | | |
|---------------------|----------------------------------|--------------------|--------|--------|--------|---------|---------|---------|----------|----------|----------|-----------|-----------|------|--|
| | | 1:1000 | 1:2000 | 1:4000 | 1:8000 | 1:16000 | 1:32000 | 1:64000 | 1:128000 | 1:256000 | 1:512000 | 1:1024000 | 1:2048000 | | |
| 08E (#632-24) | Preimmune sera (#2576L):11/10/99 | 0.13 | 0.09 | 0.08 | 0.07 | 0.07 | 0.07 | 0.07 | 0.06 | 0.07 | 0.07 | 0.07 | 0.07 | 0.07 | |
| | Average | 0.10 | 0.08 | 0.07 | 0.07 | 0.07 | 0.07 | 0.07 | 0.06 | 0.06 | 0.07 | 0.06 | 0.07 | 0.07 | |
| | α -08E (#2576K):1/11/2000 | 0.11 | 0.08 | 0.07 | 0.07 | 0.07 | 0.07 | 0.07 | 0.06 | 0.07 | 0.07 | 0.06 | 0.07 | 0.07 | |
| | Average | 2.92 | 2.81 | 2.74 | 2.70 | 2.58 | 2.08 | 1.61 | 1.01 | 0.68 | 0.40 | 0.24 | 0.15 | 0.15 | |
| | Preimmune sera (#2333L):11/10/99 | 2.93 | 2.77 | 2.74 | 2.69 | 2.48 | 2.08 | 1.57 | 1.00 | 0.66 | 0.40 | 0.23 | 0.16 | 0.16 | |
| | Average | 2.93 | 2.79 | 2.74 | 2.69 | 2.53 | 2.08 | 1.59 | 1.00 | 0.67 | 0.40 | 0.23 | 0.16 | 0.16 | |
| | Preimmune sera (#2333L):11/10/99 | 0.09 | 0.07 | 0.06 | 0.06 | 0.07 | 0.07 | 0.07 | 0.07 | 0.07 | 0.07 | 0.07 | 0.07 | 0.07 | |
| | Average | 0.08 | 0.07 | 0.06 | 0.07 | 0.10 | 0.07 | 0.07 | 0.07 | 0.07 | 0.07 | 0.07 | 0.07 | 0.07 | |
| | α -08E (#2333L):1/11/2000 | 0.08 | 0.07 | 0.06 | 0.06 | 0.08 | 0.07 | 0.07 | 0.07 | 0.07 | 0.07 | 0.07 | 0.07 | 0.07 | |
| | Average | 2.73 | 2.75 | 2.64 | 2.48 | 2.30 | 1.78 | 1.41 | 0.92 | 0.58 | 0.32 | 0.20 | 0.14 | 0.14 | |
| | | 2.73 | 2.76 | 2.51 | 2.60 | 2.37 | 1.93 | 1.44 | 0.88 | 0.58 | 0.35 | 0.20 | 0.14 | 0.14 | |
| | | 2.73 | 2.76 | 2.57 | 2.54 | 2.33 | 1.85 | 1.43 | 0.90 | 0.58 | 0.33 | 0.20 | 0.14 | 0.14 | |

Fig. 23

affi-pure O8E #2576L 739.87A&B

| Date: 5/2/2000 | | | | | | | | | | | | | |
|------------------------|--|--|--|----------|--|--|--|--|--|--|--|--|--|
| Antibody Name | | O8E polyclonal | | | | | | | | | | | |
| Rabbit #, Bleed Date | | 2576L, 1/11/2000 | | | | | | | | | | | |
| Purification Method | | affinity | | | | | | | | | | | |
| Buffer | | PBS | | | | | | | | | | | |
| Notebook | | #705, p150 | | | | | | | | | | | |
| lot # | | 739.87A | | 739.87B | | | | | | | | | |
| Antibody Concentration | | 1.4mg/ml | | 1.7mg/ml | | | | | | | | | |
| Initial Amount | | 18mg | | 3mg | | | | | | | | | |
| Antigen | | Sera Sample | | | | | | | | | | | |
| on Plate | | | | | | | | | | | | | |
| O8E | | preimmune sera (2576L) | | | | | | | | | | | |
| #632-24 | | Average | | | | | | | | | | | |
| | | α -O8E (2576K):2/8/2000 | | | | | | | | | | | |
| | | Average | | | | | | | | | | | |
| | | affinity pure α -O8E poly | | | | | | | | | | | |
| | | salt peak 739-87A | | | | | | | | | | | |
| | | Average | | | | | | | | | | | |
| | | affinity pure α -O8E poly | | | | | | | | | | | |
| | | acid peak 739-67B | | | | | | | | | | | |
| | | Average | | | | | | | | | | | |
| | | 1:1000 1:2000 1:4000 1:8000 1:16000 1:32000 1:64000 1:128000 1:256000 1:512000 1:1024000 1:2048000 | | | | | | | | | | | |
| | | 0.15 0.11 0.09 0.08 0.08 0.08 0.08 0.07 0.07 0.07 0.07 0.07 | | | | | | | | | | | |
| | | 0.14 0.10 0.09 0.08 0.08 0.08 0.07 0.07 0.07 0.07 0.07 0.07 | | | | | | | | | | | |
| | | 0.14 0.10 0.09 0.08 0.08 0.08 0.07 0.07 0.07 0.07 0.07 0.07 | | | | | | | | | | | |
| | | 2.74 2.71 2.63 2.49 2.29 2.29 2.29 2.29 2.29 2.29 2.29 2.29 | | | | | | | | | | | |
| | | 2.72 2.68 2.64 2.47 2.26 2.26 2.26 2.26 2.26 2.26 2.26 2.26 | | | | | | | | | | | |
| | | 2.73 2.70 2.63 2.48 2.27 2.27 2.27 2.27 2.27 2.27 2.27 2.27 | | | | | | | | | | | |
| | | 2.69 2.60 2.50 2.21 1.83 1.83 1.83 1.83 1.83 1.83 1.83 1.83 | | | | | | | | | | | |
| | | 2.59 2.48 2.38 2.21 1.82 1.82 1.82 1.82 1.82 1.82 1.82 1.82 | | | | | | | | | | | |
| | | 2.64 2.54 2.44 2.21 1.83 1.83 1.83 1.83 1.83 1.83 1.83 1.83 | | | | | | | | | | | |
| | | 2.46 2.39 2.40 2.34 2.08 2.08 2.08 2.08 2.08 2.08 2.08 2.08 | | | | | | | | | | | |
| | | 2.65 2.66 2.61 2.45 2.14 2.14 2.14 2.14 2.14 2.14 2.14 2.14 | | | | | | | | | | | |
| | | 2.56 2.53 2.51 2.39 2.11 2.11 2.11 2.11 2.11 2.11 2.11 2.11 | | | | | | | | | | | |

Fig. 24

Anti-O8E mAb Binding to O8E Amino Acids
61-80 Induces Ligand Internalization

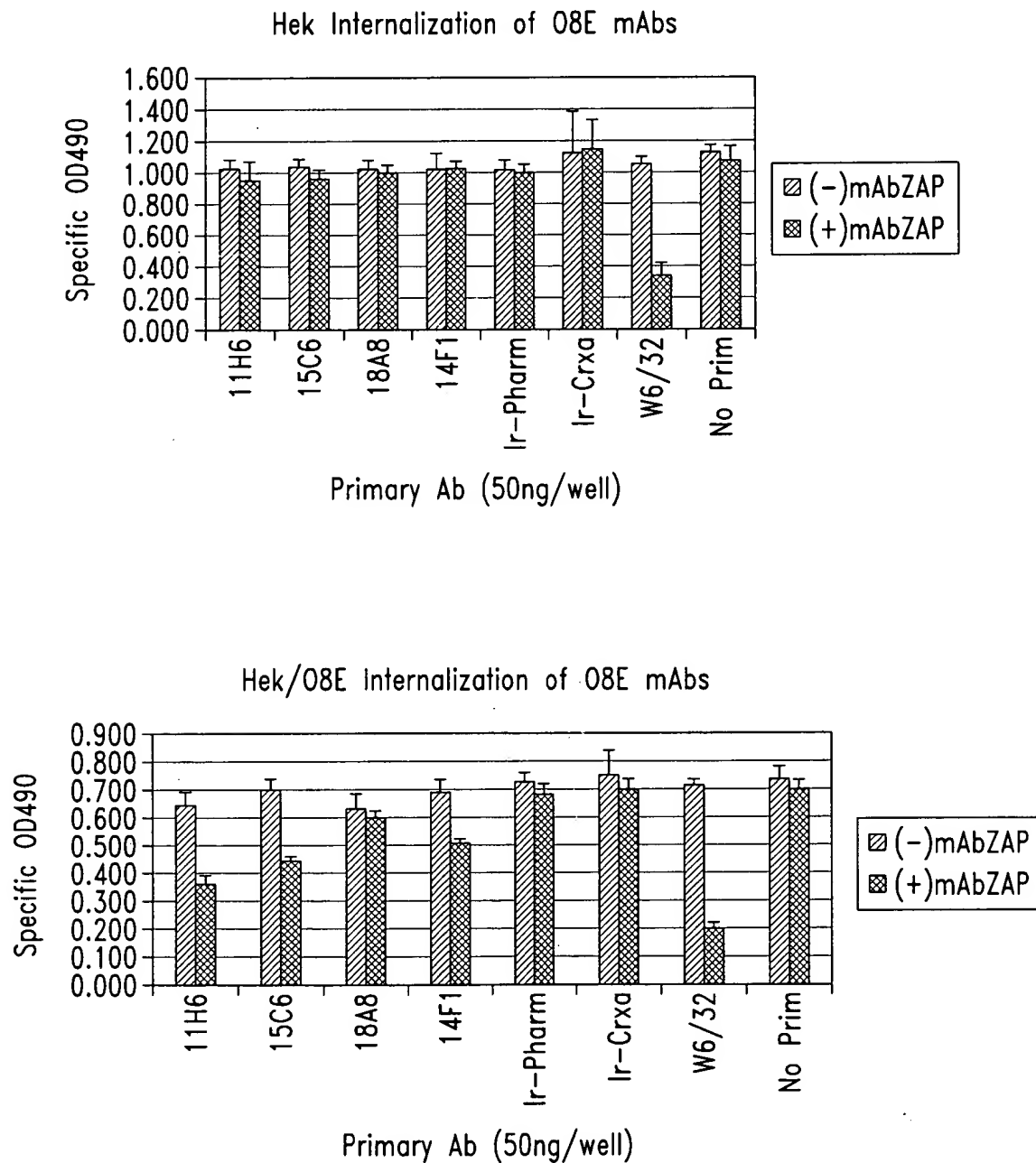


Fig. 25